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Methylophilaceae and Hyphomicrobium as target taxonomic groups in monitoring the function of methanol-fed denitrification biofilters in municipal wastewater treatment plants

Antti J. Rissanen¹,², *, Anne Ojala³,⁴, Tommi Fred⁵, Jyrki Toivonen⁶ & Marja Tiirola²

¹Department of Chemistry and Bioengineering, Tampere University of Technology, P.O. Box 541, FI-33101, Tampere, Finland
²Department of Biological and Environmental Science, University of Jyväskylä, P.O. Box 35, FI-40014, University of Jyväskylä, Finland
³Department of Environmental Sciences, University of Helsinki, P.O. Box 65, FI-00014, University of Helsinki, Finland
⁴Department of Forest Sciences, University of Helsinki, P.O. Box 27, FI-00014, University of Helsinki, Finland
⁵Helsinki Region Environmental Services Authority HSY, P.O. Box 100, FI-00066 HSY, Finland
⁶Salon Vesi, P.O. Box 77, FI-24101 Salo, Finland

*Corresponding author.
email address: antti.rissanen@tut.fi
tel. : +358 40 1981145
fax.: +358 3 3641392

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Abstract

Molecular monitoring of bacterial communities can explain and predict the stability of bioprocesses in varying physicochemical conditions. To study methanol-fed denitrification biofilters of municipal wastewater treatment plants, bacterial communities of two full-scale biofilters were compared through fingerprinting and sequencing of the 16S rRNA genes. Additionally, 16S rRNA gene fingerprinting was used for 10-week temporal monitoring of the bacterial community in one of the biofilters. Combining the data with previous study results, the family Methylophilaceae and genus Hyphomicrobium were determined as suitable target groups for monitoring. An increase in the relative abundance of Hyphomicrobium-related biomarkers occurred simultaneously with increases in water flow, NO$_x$ load, and methanol addition, as well as a higher denitrification rate, although the dominating biomarkers linked to Methylophilaceae showed an opposite pattern. The results indicate that during increased loading, stability of the bioprocess is maintained by selection of more efficient denitrifier populations, and this progress can be analyzed using simple molecular fingerprinting.

Keywords Methanol · Denitrification · Biofilter · Hyphomicrobium · Methylophilaceae
**Introduction**

Denitrification is an essential biotechnological process in municipal wastewater treatment plants (WWTPs) for reducing the nitrogen (N) load to recipient waters. This step-wise reduction of water-soluble nitrate (NO$_3^-$) via nitrite (NO$_2^-$) to gaseous nitric oxide (NO), nitrous oxide (N$_2$O), and di-nitrogen (N$_2$) is catalyzed by facultative anaerobic heterotrophic bacteria. Denitrification is a community process, as many denitrifiers perform only a portion of the reduction steps, reducing NO$_3^-$ to NO$_2^-$ or to N$_2$O, and only some bacterial species are capable of the whole denitrification chain from NO$_3^-$ to N$_2$ gas [8]. Due to the unfavorably low carbon-to-nitrogen (C:N) ratio of the water in many N removal systems, an additional organic C and energy source, usually methanol, is used in the process. In WWTPs, methanol-fed denitrification is often accomplished by filtration of the wastewater through a support material in biofilters [17].

The physicochemical and technical aspects of the methanol-utilizing denitrification processes have been comprehensively characterized [17, 20]. However, the optimal control and operation of the processes would also benefit greatly from microbiological data [22, 39], such as the identity and potential controlling factors of the taxonomic groups crucial for the system function, which could be used in process monitoring [22]. Methylotrophs play a key role in methanol-fed denitrification systems, both by directly utilizing methanol as an electron donor in denitrification as well as by transforming methanol into various organic extracellular compounds, which are utilized by co-occurring non-methylotrophic denitrifiers [22]. Of the known methylotrophic denitrifiers, the genus *Hyphomicrobium* (*Alphaproteobacteria*) is frequently detected in methanol-fed denitrification systems [2, 6, 21, 27-29, 35, 38] and is thus considered a suitable target for monitoring methanol-fed denitrification [22]. In addition, bacteria
within family *Methylophilaceae* (*Betaproteobacteria*) [10, 29, 33, 36] as well as within genera *Methyloversatilis* (*Betaproteobacteria*) [2] and *Paracoccus* (*Alphaproteobacteria*) [6, 21, 27] can also play a significant role in the process.

However, most studies have been done at laboratory scale. Other than the studies of Neef et al. [27] and Lemmer et al. [21], which found *Paracoccus* and *Hyphomicrobium* to be important methylotrophs in a methanol-fed denitrifying sand filter of a WWTP, very little is known about the overall bacterial dynamics or about the identity and community dynamics of methylotrophic denitrifiers in full-scale biofilters. There are ecological differences between methylotrophs and non-methylotrophs [21]. In addition, the ecology of *Hyphomicrobium* differs from that of *Methyloversatilis* [2], *Paracoccus* [21], and *Methylophilaceae* [10]. This indicates that methylotrophs and non-methylotrophs as well as different taxonomic groups of methylotrophs respond differently to the temporal and inter-system variations in the physicochemical conditions confronted by the full-scale biofilters.

This study investigated the bacterial communities of two full-scale methanol-fed denitrifying WWTP biofilters by length heterogeneity PCR (LH-PCR) [37] and clone library and 454-pyrosequencing analysis of the 16S rRNA gene sequences. We specifically focused on the taxonomic groups of the methylotrophic bacteria that inhabited both of the biofilters as well as previously studied systems. In addition to comparing the bacterial communities of the two biofilters, we analyzed the temporal variation in the structure of the bacterial communities and linked it with the physicochemical and functional data during a 10-week follow-up period in one of the biofilters. We aimed to determine the following: 1) which methylotrophic taxonomic groups are typical for methanol-fed denitrification systems and could thus be used as target taxonomic groups for monitoring the process function in full-scale WWTP
biofilters; 2) whether variations in physicochemical conditions affect the bacterial community structure; and 3) whether methylotrophs and non-methylotrophs as well as 4) different taxonomic groups of methylotrophs respond differently to these variations.

**Materials and methods**

**Microbiological sampling**

Samples were collected from the methanol-fed denitrification filters of two municipal wastewater treatment plants: the Viikinmäki wastewater treatment plant in Helsinki, Finland (WWTPA), and the Salo wastewater treatment plant in Salo, Finland (WWTPB) (Table 1). WWTPA is a large plant with one of the largest denitrification filter systems in the world, whereas WWTPB is a small-sized plant (Table 1).

Methanol-fed denitrification filters have been functioning since 2004 and 2007 in WWTPA and WWTPB, respectively. In both sites, the denitrification is preceded by an aerobic stage (activated sludge) where nitrification occurs. The samples from the denitrification filter of WWTPA were collected from the same denitrification cell at 5 to 9 day intervals during a 10-week follow-up period (27 August 2008 – 28 October 2008). The samples from the denitrification filter of WWTPB were collected once (2 October 2008). In addition, samples from the inflow of the denitrification systems were collected once (from WWTPA 10 November 2008 and from WWTPB 2 October 2008).

The biofilter samples were taken from the backwash water channel.

Backwashing consists of air-sparging and washing, which detaches biomass from the carrier material. Samples of the backwash water (1 sample per sampling date in WWTPA, 2 replicate samples in WWTPB) and polystyrene carrier material beads escaping from the WWTPB biofilter were collected into sterile 50 ml plastic containers. Bacteria in the inflow of the systems were collected by filtering 100–200 ml water using
Sarstedt Filtropur S 0.2 polyethersulfone filters. The samples were stored at -20 °C before further processing within 1 to 2 months.

**Background data and NO\textsubscript{x} reduction**

Online monitoring data of the WWTPs were used as background data in this study. For WWTPA, water flow (W\textsubscript{f}), methanol addition rate (Met\textsubscript{f}), inflow and outflow concentrations of NO\textsubscript{3}\textsuperscript{-}+NO\textsubscript{2}\textsuperscript{-} (henceforth NO\textsubscript{x} in and NO\textsubscript{x} out, respectively) in the studied denitrification cell, as well as inflow temperature (T) and inflow concentrations of O\textsubscript{2} (O\textsubscript{2in}), suspended solids (SS\textsubscript{in}), PO\textsubscript{4}\textsuperscript{3-} (PO\textsubscript{4}\textsubscript{3-\textsubscript{in}}), total phosphorous (TP\textsubscript{in}) and outflow concentrations of SS (SS\textsubscript{out}), PO\textsubscript{4}\textsuperscript{3-} (PO\textsubscript{4}\textsubscript{3-\textsubscript{out}}), and TP (TP\textsubscript{out}) in the whole denitrification system were measured hourly. Daily averages (for the time period 20 August 2008 – 31 October 2008) were then calculated. For WWTPB, daily averages (for the time period 1 September 2008 – 31 October 2008) for W\textsubscript{f} and Met\textsubscript{f} along with T, NO\textsubscript{x} in, PO\textsubscript{4}\textsuperscript{3-\textsubscript{in}}, SS\textsubscript{in}, and O\textsubscript{2in} and NO\textsubscript{x} out, PO\textsubscript{4}\textsubscript{3-\textsubscript{out}}, and SS\textsubscript{out} were calculated for the whole denitrification system. The NO\textsubscript{x} load (µmol s\textsuperscript{-1}) in the inflow (tNO\textsubscript{x} in) and outflow (tNO\textsubscript{x} out) water was calculated from W\textsubscript{f} and NO\textsubscript{x} in or NO\textsubscript{x} out. Denitrification in the filters was calculated either as relative (%) or actual (µmol s\textsuperscript{-1}) NO\textsubscript{x} reduction as follows:

\[
NO\textsubscript{x} \text{ reduction} = \frac{(NO\textsubscript{x} \text{ in} - NO\textsubscript{x} \text{ out})}{NO\textsubscript{x} \text{ in}} \times 100
\]

\[
\text{Actual } NO\textsubscript{x} \text{ reduction} = tNO\textsubscript{x} \text{ in} - tNO\textsubscript{x} \text{ out}
\]

Denitrification in this study refers to the conversion of water soluble NO\textsubscript{x} into gaseous forms, but the proportions of NO, N\textsubscript{2}O, and N\textsubscript{2} in the end product are not separated.

**Molecular microbiological analyses**
DNA extraction of each sample – from 10 mg of freeze-dried backwash sample material from WWTPA and WWTPB, from 5 frozen carrier beads from WWTPB (sample WWTPB_Car), and from the Filtropur filters containing the inflow water samples – was carried out as previously described [32].

For the LH-PCR analysis, PCR was performed using the universal bacterial primers F8 (5´-AGA GTT TGA TCM TGG CTC AG-3´) (1:4 ird700-labelled) [41] and PRUN518r (5´-ATT ACC GCG GCT GCT GG-3´) [26], with a GeneAmp PCR system 9600 (Perkin Elmer), in previously described reaction mixtures [31]. For the PCR reaction, the following program was used: an initial denaturation step at 95°C for 5 min, 30 cycles of amplification (94°C for 30 s, 53°C for 1 min, 72°C for 3 min), and final elongation at 72°C for 15 min. The LH-PCR analysis was done as previously described [31]. The relative area (%), that is, the relative abundance of each LH-PCR peak was defined as a ratio of the total peak area (sum of the areas of all peaks) of the sample.

PCR for the clone library analyses of 16S rRNA was performed using the universal bacterial primers 27F (5´- AGAGTTTGATCMTGGCTCAG - 3´) [19] and 907R (5´- CCGTCAATTCMTTGGAGT - 3´) [13], and cloning and sequencing (Sanger sequencing) of the PCR amplicons was done as in Rissanen et al. [32]. For the clone libraries, PCR products of the samples from WWTPA on all sampling dates (WWTPA - library), PCR products of the replicate samples of backwash water (WWTPB - library), and the carrier materials of WWTPB (WWTPB_Car - library) were pooled separately.

The bacterial communities of WWTPA were also studied via 454-pyrosequencing. Equal amounts of nucleic acid extracts from each sampling date were pooled before PCR reactions, and the PCR and sequencing was performed as previously described [32].
Sequence analysis

The analysis of the clone library and 454-pyrosequencing library sequences was done as previously described [32]. Putative methylotrophic operational taxonomic units (OTUs) (97 % identity threshold) were determined based on the previous literature [1, 2, 5, 10, 18, 27, 34-35]. Clone library OTUs assigned to the methylotrophic families found from both biofilters (Methylophilaceae and Hyphomicrobiaceae) were subjected to phylogenetic tree analyses, as described previously [32]. In addition, phylogenetic classification was linked to the LH-PCR peaks in silico using the length and taxonomical data obtained in the clone library analysis.

16S rRNA gene sequences of the clone libraries were deposited into the EMBL database (accession numbers KP098594 – KP098735, KP098971 – KP098975, and KP098985 – KP098988). The 454-pyrosequencing data were deposited into the NCBI SRA database (SRX646346).

Statistical analyses

Bray–Curtis dissimilarities among the samples were calculated from the relative abundances of the LH-PCR peaks. Temporal variations in the structure of the bacterial communities of WWTPA were then analyzed by non-metric multidimensional scaling (NMS) of the LH-PCR peak data. Changes in the WWTPA community structures were correlated with variations in the background parameters using Mantel’s test. In addition, temporal variations in the relative abundances of the LH-PCR peaks affiliated with methylotrophs and non-methylotrophs were correlated with variations in the background parameters using either Pearson correlation analysis (for normally distributed variables, normality tested using the Shapiro–Wilk test) or Spearman’s
correlation analysis (for non-normally distributed variables). For background parameters, the average daily values for the time period between the two samplings was used in the correlation analyses. Temporal and inter-system variations in the community structures were also analyzed by hierarchical clustering (UPGMA linkage) using the LH-PCR data. The NMS analysis and Mantel’s test were performed in PC-ORD 6.0 [24], and cluster analysis was done using PAST version 3.09 [11]. The correlation analyses were performed in PASW 18.0 (PASW Statistics 18, Release Version 18.0.0, SPSS, Inc., 2009, Chicago).

**Results**

**Performance of the denitrification biofilters**

As is typical for WWTPs in Northern countries in autumn, $W_f$ increased and $T$ decreased during the study period in both filter systems (Fig. 1, Online Resource 1).

$\text{NO}_x^\text{in}$ and $\text{O}_2^\text{in}$ were generally higher and more variable in WWTPB ($\text{NO}_x^\text{in}$: 700 – 2900 µmol/L; $\text{O}_2^\text{in}$: 1 to 215 µmol/L) than in WWTPA ($\text{NO}_x^\text{in}$: 500 – 1000 µmol/L; $\text{O}_2^\text{in}$: 40 - 110 µmol/L). In addition, $\text{NO}_x^\text{in}$ decreased in WWTPB and $\text{O}_2^\text{in}$ in WWTPA during the study period (Fig. 1, Online Resource 1). The higher $\text{NO}_x^\text{in}$ in WWTPB compared to WWTPA could be due to possible differences in the total N concentrations feeding the WWTPs, the nitrification efficiency between WWTPA and WWTPB, or the lack of a pre-denitrification system in WWTPB (Table 1). In the filters, Met$_f$ is controlled by a feedback loop that controls the $\text{NO}_3^\text{-N}$ concentration inside the filter cells [7]. As a result, Met$_f$ followed $\text{NO}_x^\text{in}$ tightly, and they both controlled the actual $\text{NO}_x^\text{r}$ reduction rate ($\mu$mol/s) in the systems (Fig. 1, Online Resource 1). This kept the C:N ratio in the inflow (Met$_f$: $\text{NO}_x^\text{in}$ ratio), as well as the relative $\text{NO}_x^\text{r}$ reduction and the $\text{NO}_x^\text{r}$ out concentration, relatively stable in both systems. However, the relative $\text{NO}_x^\text{r}$ reduction and $\text{NO}_x^\text{r}$ out concentration were higher and lower, respectively, and
temporally more stable, and Metf:1NO\(_x\)-inflow was lower in WWTPA (Metf:1NO\(_x\)-inflow ratio: 0.90–1.13; relative NO\(_x\)- reduction: 82–93 %; NO\(_x\)-out: 66–99 µmol/L) than in WWTPB (Metf:1NO\(_x\)-inflow ratio: 0.98–1.18; relative NO\(_x\)- reduction: 64–90 %; NO\(_x\)-out: 128–870 µmol/L, when the exceptional values of 25 October were excluded) (Fig. 1, Online Resource 1). When estimated per carrier volume, the load of NO\(_x\), O\(_2\) and methanol feeding as well as the actual NO\(_x\)-reduction rate were on average lower in WWTPA (NO\(_x\): 570 µmol/m\(^3\)/s; O\(_2\): 50 µmol/m\(^3\)/s; methanol: 590 µmol/m\(^3\)/s; actual NO\(_x\)-reduction: 510 µmol/m\(^3\)/s) than in WWTPB (NO\(_x\): 890 µmol/m\(^3\)/s; O\(_2\): 60 µmol/m\(^3\)/s; methanol: 930 µmol/m\(^3\)/s; actual NO\(_x\)-reduction: 730 µmol/m\(^3\)/s). The higher O\(_2\) load increases the requirement for electron donors for O\(_2\) reduction (to allow anaerobic conditions for denitrification), which explains the higher Metf:1NO\(_x\)-inflow ratio in WWTPB than in WWTPA. Furthermore, the average surface load was higher and the average hydraulic retention time (HRT) lower in the biofilter of WWTPA (Table 1).

**Differences in the bacterial community structures between the biofilters**

Based on the UPGMA clustering of the LH-PCR data, conditions within the biofilters shaped the original bacterial communities (communities of the inflow water) in both WWTPA and WWTPB (Online Resource 2 & 3). The bacterial communities of the WWTPA and WWTPB samples clustered separately (Table 2, Online Resource 2 & 3), except for the carrier material of WWTPB, which more resembled the backwash water of WWTPA than that of WWTPB (Table 2, Online Resource 2).

Samples of the sheared biomass in the backwash water were used in comparing the methylotrophic communities between WWTPA and WWTPB. The relative abundance of putative methylotrophs was much higher in WWTPB than in WWTPA.
Methylophilaceae and Hyphomicrobiaceae were the dominant methylo trophic families that were found in both biofilters, whereas Paracoccus (Rhodobacteraceae) and Methyloversatilis (Rhodocyclaceae) were found only in WWTPB (Table 2, Figs. 2-3). According to the clone library analyses, Hyphomicrobiaceae had a much higher relative abundance in WWTPA than in WWTPB, whereas the opposite was observed for Methylophilaceae (Table 2). In contrast to the backwash sample, the carrier material of WWTPB did not harbor Paracoccus or Methyloversatilis but rather Bradyrhizobium. The carrier material of WWTPB also had a higher and lower relative abundance of Hyphomicrobiaceae and Methylophilaceae, respectively, than the backwash material of WWTPB (Table 2).

Hyphomicrobiaceae was represented by only 2 OTUs in the clone libraries. These OTUs belonged to Hyphomicrobium cluster II [30] (Table 2, Fig. 2). OTU 16 was shared between WWTPA and WWTPB. The other OTU, OTU 22, likely representing a different Hyphomicrobium species, was only found in the carrier material of WWTPB (Fig. 2), where it was more abundant than OTU 16. 454-pyrosequencing had a lower resolution for detecting Hyphomicrobiaceae than the clone library analysis (Table 2), but it showed 7 Hyphomicrobiaceae OTUs in WWTPA, of which the dominant one, harboring almost all (91 %) of the Hyphomicrobiaceae sequences in the 454-pyrosequencing library, was identical to OTU 16 in the clone library (Fig. 2).

Bacteria within Methylophilaceae, consisting of 10 OTUs, were divided into four groups (Table 2, Fig. 3). Three of the groups, that is, clusters Met I, Methylotenera I, and Methylotenera II (clustering according to this study), included 8 OTUs covering the majority of the observed Methylophilaceae sequences (Table 2, Fig. 3). Methylotenera I and Methylotenera II were closely related to the cultured members of the genus Methylophilaceae (Fig. 3), while the Met I cluster probably represented a novel species of
Methylotenera with no cultured representatives so far. The fourth group included two rare OTUs that were not closely affiliated to known Methylophilaceae genera (Table 2, Fig. 3). Strikingly, despite the high relative abundance of Methylophilaceae, the backwash material of WWTPB had only one Methylophilaceae OTU, and it belonged to cluster Met I (Fig. 3). Cluster Met I was also the most abundant group of Methylophilaceae in the carrier material of WWTPB, whereas it was absent in WWTPA (Table 2, Fig. 3). In contrast, clusters Methylotenera I and II were found in the backwash material of WWTPA and also in the carrier material of WWTPB (Table 2, Fig. 3). Methylotenera I was much more abundant than Methylotenera II in WWTPA, but it was only slightly less abundant than Methylotenera II in the carrier material of WWTPB (Table 2). 454-pyrosequencing found 6 Methylophilaceae OTUs in WWTPA, of which the dominant OTU, harboring almost all (99%) of the Methylophilaceae sequences in the 454-pyrosequencing library, was identical to Methylotenera OTU 6 (within cluster Methylotenera I) in the clone library analyses (Fig. 3). Furthermore, 454-pyrosequencing of 16S rRNA gene amplicons revealed a marginal abundance (≤1% of 16S rRNA sequences) of the following putative methylotrophs: Methylocystaceae, Methylococcaceae, Acinetobacter, and Flavobacterium in WWTPA (Table 2). 454-pyrosequencing also resulted in a higher proportion of unclassified bacterial sequences than the clone library analysis (Table 2).

The abundant non-methylotrophic bacterial groups (≥5% of 16S rRNA sequences in any of the libraries) included Acidobacteria, Actinobacteria, Bacteroidetes (other than Flavobacterium), Chloroflexi, Comamonadaceae, Deltaproteobacteria, Planctomycetes, and Rhodocyclaceae (other than Methyloversatilis) (Table 2).

Temporal variation in the bacterial community in the WWTPA biofilter
The bacterial community structure changed over time (non-metric multidimensional scaling analysis, Fig. 1), along with a temporal change in several operational parameters (Fig. 1). The fluctuations in the community structure were correlated with variations in $W_f$ (Mantel’s test, $r = 0.36$, $p < 0.05$, $n = 10$), $\Delta \text{NO}_x\text{in}$ ($r = 0.61$, $p < 0.05$, $n = 10$), $\text{Mef}$ ($r = 0.55$, $p < 0.05$, $n = 10$), and $T$ ($r = 0.59$, $p < 0.05$, $n = 10$). In addition, the community structure correlated with the actual NO$_x$ reduction rate ($r = 0.62$, $p < 0.05$).

To study the variation of the methylotrophic taxa in WWTPA, the phylogenetic classification was linked to the LH-PCR peaks in silico using the length and taxonomic data obtained from the clone library analyses (Online Resource 3). All the clone library sequences with a size of 466 bp in the area amplifiable by LH-PCR primers belonged to OTU 16 within the *Hyphomicrobium* II cluster, and all the sequences of genus *Hyphomicrobium* had the size of this peak (see Fig. 2). The sequences assigned to *Methylophilaceae* were found only within peaks 521 bp and 524 bp, and they dominated only within peak 521 bp (73 %), which was also the largest peak in the LH-PCR profiles of WWTPA (Online Resource 3). Peak 521 bp consisted mostly of OTU 6 within the *Methylophilaceae* I cluster (67 %) and for the smaller part of the unclassified *Methylophilaceae* OTU 137 (6 %) (see Fig. 3), *Burkholderiales* (13 %), *Rhodocyclales* (7 %, not *Methyloversatilis*), and *Bacteroidetes* (7%, not *Flavobacterium*). Thus, LH-PCR peaks 466 bp and 521 bp were chosen as biomarkers of *Hyphomicrobium* and *Methylophilaceae*, respectively. Furthermore, the sum of LH-PCR peaks 466 bp and 521 bp were used as a general biomarker for methylotrophs, whereas the sum of all peaks excluding methylotrophic peaks 466 bp, 521 bp, and 524 bp (see above) were used as a biomarker for non-methylotrophs.

During the study period, there was a negative correlation between the relative abundances of *Hyphomicrobium* and *Methylophilaceae* ($r = -0.91$, $p < 0.001$) (Fig. 4).
The relative abundance of *Hyphomicrobium* increased as *Met*ₚ, *W*ₚ, and *lNOₓ in* increased (Metₚ: r = 0.74, p < 0.05; Wₚ, ρ = 0.67, p < 0.05; lNOₓ in, r = 0.80, p < 0.05, n = 10) (Figs. 1 & 4), while the opposite took place with *Methylophilaceae* (Metₚ: r = -0.74, p < 0.05; Wₚ, ρ = -0.66, p < 0.05; lNOₓ in, r = -0.77, p < 0.05, n = 10). The relative abundance of *Methylophilaceae* also increased as *T* increased (r = 0.67, p < 0.05, n = 10), while there was no correlation between *T* and *Hyphomicrobium* (r = -0.62, p = 0.06, n = 10) (Fig. 4). The relative abundance of total methylotrophs decreased as *Met*ₚ and *lNOₓ in* increased (Metₚ: r = -0.73, p < 0.05; lNOₓ in, r = -0.77, p < 0.05, n = 10) and *T* decreased (r = 0.67, p < 0.05), while the opposite took place with non-methylotrophs (Metₚ: r = 0.79, p < 0.05; lNOₓ in: r = 0.80, p < 0.05; T: r = -0.72, p < 0.05, n = 10) (Fig. 4). An increase in the relative abundance of *Hyphomicrobium* (r = 0.77, p < 0.05, n = 10) and non-methylotrophs (r = 0.80, p < 0.05, n = 10) and a decrease in *Methylophilaceae* (r = -0.77, p < 0.05, n = 10) and total methylotrophs (r = -0.76, p < 0.05, n = 10) also occurred with the increase in the actual NOₓ⁻ reduction rate (Figs. 1 & 4).

**Discussion**

Bacteria belonging to genus *Hyphomicrobium* inhabited both WWTP biofilters. This agrees with the results from many previous studies [e.g. 2, 27, 29] indicating that bacteria in *Hyphomicrobium* are crucial for the function of methanol-utilizing denitrification processes. Moreover, this further confirms that *Hyphomicrobium* is a suitable target genus for monitoring denitrification in full-scale methanol-fed WWTP biofilters [23].

*Methylophilaceae* were also important components of the bacterial communities in both biofilters, which is in accordance with results from laboratory-scale methanol-
fed denitrification systems [10, 29, 36]. In addition, *Methylophilaceae* were abundant in 
pilot-scale activated sludge reactors during a period of high nitrate and methanol 
concentration [12] and in a full-scale, methanol-fed, activated sludge plant [33]. Since 
the first indication of the methylotrophic denitrification capability of *Methylophilaceae* 
was shown in 2004 [10], *Methylophilaceae* were not even targeted (*Methylophilaceae-* 
specific fluorescence *in situ* hybridized [FISH] probes were not used) in a previous 
study of a full-scale WWTP biofilter (a sand filter) [21, 27]. However, the addition of 
methanol led to enrichment of *Betaproteobacteria* in the biofilter [27], and it can be 
suggested that this was at least partially due to the growth of *Methylophilaceae*.
Together, these results suggest that, besides *Hyphomicrobium*, bacteria belonging to 
*Methylophilaceae* are crucial for the function of methanol-utilizing denitrification 
processes. Furthermore, the results from the WWTPA and WWTPB biofilters and 
methanol-affected activated sludge systems [12, 33] indicate that, of the family 
*Methylophilaceae*, the bacteria belonging to genus *Methylotenera*, which includes 
species that couple methylotrophs to denitrification [16], can be important components 
of methanol-fed denitrification systems. In addition, many yet uncultivated species of 
*Methylotenera* probably also exist, as exemplified by the abundant Cluster Met I 
detected in WWTPB. However, *Methlobacillus* [29, 36] and *Methylophilus* [29] as 
well as another, thus far uncultivated *Methylophilaceae* genus [10] (Fig. 3) were 
determined to be the primary methanol-consuming *Methylophilaceae* in previous 
laboratory-scale studies of methanol-utilizing denitrification. Thus, *Methylophilaceae* 
can be used as a target family for monitoring denitrification in full-scale methanol-fed 
WWTP biofilters, although there can be variation in the genera and species mediating 
the process between different systems.
The considerable differences between the bacterial communities within the biofilters and in the water feeding the biofilters indicate that prevailing physicochemical conditions are very strong determinants of the bacterial community structure inside the biofilters. A change in the primary C source from multicarbon sources (present in the feed water) to methanol can exert an especially strong structuring force on the bacterial communities [36]. We suggest that differences in the biofilter communities between WWTPA and WWTPB are mostly due to variations in physicochemical conditions, but the effect of variations in the original inocula (bacteria from preceding activated sludge stage) cannot be completely ruled out.

Many possible physicochemical factors might have affected the differences between the filters. The higher abundance of methylotrophs in WWTPB than in WWTPA could be explained by the higher availability of methanol (higher Met\(_f\):LNO\(_x\) infiltration and higher Met\(_f\) estimated per carrier volume). As a higher O\(_2\) load caused the higher Met\(_f\):LNO\(_x\) infiltration in WWTPB, the higher abundance of methylotrophs could be due to a higher contribution of aerobic methylotrophs and methylotrophs performing aerobic denitrification in WWTPB. Analogous to aerobic methane oxidation coupled with denitrification (AME-D) [43], these methylotrophs could have contributed to the overall denitrification performance by consuming O\(_2\) and by converting methanol to substrates utilizable by non-methylotrophic denitrifiers. However, higher HRT and lower surface load, which act through decreasing the input of bacteria (mostly non-methylotrophic) from the preceding activated sludge stage and through lowering the physical force exerted on the carrier material, might have also favored the growth and development of methylotrophs over non-methylotrophs in WWTPB.

Capable of aerobic denitrification, *Paracoccus* tolerates O\(_2\) better than *Hyphomicrobium*, which thrive in anoxic conditions, and thus *Paracoccus* were favored...
in the surface zones of the biofilm in a previously studied full-scale biofilter (a sand filter) [21]. This is in accordance with our results on the higher and lower relative abundance of *Paracoccus* and *Hyphomicrobium*, respectively, in the sheared biomass of the backwash water (representing more aerobic surface biofilm) than in the carrier material (representing deeper anoxic biofilm) in WWTPB. Similarly, the lower O$_2$ load (as expressed per carrier volume) could explain the higher abundance of *Hyphomicrobium* and the absence of *Paracoccus* in WWTPA. Since some *Methylotenera* strains are aerobic [3, 14] or perform aerobic denitrification [25], the higher abundance of *Methylophilaceae* in the sheared biomass than in the carrier material could also be due to differences in O$_2$ availability. However, it could also be due to differences in NO$_3^-$ and methanol availability, which is expected to be higher in the biofilm surface. The results indicate that Cluster Met I, which was the sole *Methylophilaceae* group in the sheared biomass of WWTPB, was especially favored by the higher availability of O$_2$, NO$_3^-$, and/or methanol. Therefore, the lower O$_2$, NO$_3^-$, and methanol load (as expressed per carrier volume) could both explain the lower abundance of *Methylophilacea* and the absence of Cluster Met I in WWTPA. However, as discussed below for the temporal variation in the bacterial community in WWTPA, the lower abundance of *Methylophilacea* and higher abundance of *Hyphomicrobium* in WWTPA could also be due to a lower HRT and higher surface load, which could favor *Hyphomicrobium* over *Methylophilacea*. In addition, as there are variations in the response of different *Hyphomicrobium* species to varying NO$_3^-$ [23], the differential distribution of the two *Hyphomicrobium* species (OTUs) between the sheared biomass and carrier material in WWTPB was probably due to the decreased availability of NO$_3^-$ deeper in the biofilm. Finally, *Methyloversatilis* and *Paracoccus* gain an ecological advantage by shifting between using C1-carbon and multicarbon substrates [2, 4, 34].
Their presence in WWTPB but not in WWTPA might also reflect higher temporal variation in the availability of methanol or higher and temporally more variable availability of other C sources (present in feed water or produced from methanol) in WWTPB.

In accordance with the results from the comparison of the biofilters, many possible physicochemical factors might have affected the temporal variation in the bacterial community structure within the WWTPA biofilter. The overall bacterial community structure changed due to variations in the availability of electron acceptors (NO\textsubscript{x}) and donors (methanol) as well as in temperature, which has also previously been shown to affect denitrifying communities [9, 40]. In addition, changes in the water flow, which act through changing the HRT and surface load, possibly affected the community structure. However, due to the covariation among these factors (Fig. 1) and the relatively small sample size, it is impossible to specify the effects of each variable. In contrast to explaining differences between the biofilters, the availability of O\textsubscript{2} (the O\textsubscript{2} concentration and the O\textsubscript{2} flow [µmol s\textsuperscript{-1}] [data not shown]) did not affect the temporal variation in the community structure in WWTPA.

Assigning taxonomies to the LH-PCR peaks allowed for analysis of the relationship between the physicochemical factors and bacterial communities at the level of major functional and methylotrophic groups. Methylotrophs and non-methylotrophs as well as the key methylotrophic groups, Methylophilaceae and Hyphomicrobium, responded differently to variations in the physicochemical factors. Since the bulk of methylotrophs consisted of Methylophilacea in every sampling occasion, the variation in the relative abundance of methylotrophs tightly followed that of Methylophilacea. The decrease in Methylophilacea (and total methylotrophs) and increase in Hyphomicrobium and non-methylotrophs with increasing NO\textsubscript{x} and methanol loads
contrasts with the above comparison between WWTPA and WWTPB. This discrepancy could be due to the dominant *Methylophilaceae* group in WWTPA, *Methylotenera* I, having a slower growth rate and a lesser response to increases in NO$_3^-$ and methanol than the dominant group in WWTPB, Cluster Met I. However, differences in the water flow acting through changes in the HRT and surface load provide a more unifying explanation for the community variations both between the biofilters and within WWTPA. With an increased water flow (lowered HRT and increased surface load), the input of non-methylotrophic bacteria from the preceding activated sludge stage was increased, which could have lowered the relative abundance of *Methylophilaceae* (and total methylotrophs). Furthermore, increased physical disturbance due to increased water flow could have caused the selective removal of *Methylophilaceae*, which would further contribute to the decrease in methylotrophs as well as to the increase in *Hyphomicrobium*. Prosthecae and buds of *Hyphomicrobium* [42] might have provided firmer attachment to the carrier material than the flagellum and ‘prostheca-like’ structures of *Methylotenera* [15]. In addition, decreased temperature could have decreased the growth rate of *Methylophilaceae* (and total methylotrophs), which could have also contributed to the observed community variations.

Physicochemical factors can control microbial process rates both directly by affecting the short-term cell function and indirectly by affecting the microbial community structure in the longer term [40]. The correlation between the community structure and function (actual NO$_3^-$ reduction rate) in the WWTPA biofilter suggests that physicochemical factors controlled the denitrification rate of the biofilter indirectly by modifying the community composition. However, this study cannot rule out the importance of direct control of physicochemical factors on cell function. The decrease in *Methylophilaceae* and total methylotrophs and increase in *Hyphomicrobium* and non-
methylotrophs with an increasing actual NO$_x$-reduction rate is surprising and contrasts with the results from a laboratory reactor in which the relative abundance of *Methylophilaceae* increased and that of *Hyphomicrobium* did not change with increasing denitrification rate [10]. However, this discrepancy is probably due to differing expressions of the process rate, expressed as per biofilter or per volume of carrier material in our study and as per mass of biomass (mixed liquor volatile suspended solids [MLVSS]) in Ginige et al. [10]. Unfortunately, MLVSS was not analyzed in this study. However, the higher actual NO$_x$-reduction rate with an increasing relative abundance of non-methylotrophs suggests that non-methylotrophs can efficiently support the N removal of methanol-fed denitrification systems, especially during periods of high N load. In those conditions, methylotrophs might have increasingly allocated more of the methanol C into extracellular substances than into biomass and thus supported the activity of non-methylotrophs.

**Conclusions**

Combining the results of the two WWTP biofilters with those of previous studies confirms that bacteria in genus *Hyphomicrobium* and family *Methylophilaceae* are crucial components of methanol-utilizing denitrification. Thus, *Hyphomicrobium* and *Methylophilaceae* can be used as target taxonomic groups to monitor the function of full-scale methanol-fed denitrification biofilters of WWTPs. Although *Methylotenera* was the major *Methylophilaceae* genus in the studied WWTP biofilters, other genera (*Methylophilus* and *Methylobacillus*) may be more important in other systems. There were differences in the bacterial communities between the biofilters. In addition, 10-week monitoring of one of the biofilters showed temporal variation in the bacterial community. Variation in the loads of NO$_x$- and O$_2$ as well as in the methanol addition
rate, water flow rate (acting through changing HRT and surface load), and temperature were all potential candidates affecting the structure of the bacterial communities. Methylotrophs and non-methylotrophs as well as *Hyphomicrobium* and *Methylophilaceae* responded differently to these variations. Furthermore, the correlation of the bacterial community structure with the process function (actual NO\textsubscript{3}⁻ reduction rate) in the temporally monitored biofilter indicates that fluctuating physicochemical conditions affected the denitrification rate indirectly by affecting the community composition. Further temporal monitoring and/or experimental studies combined with modern sophisticated culture-independent (stable isotope probing of DNA/RNA, metatranscriptomics, metagenomics) as well as culture-dependent (high-throughput culturing) techniques are needed to resolve the exact mechanisms underlying the observed relationship among the physicochemical factors, bacterial communities (methylotrophs, non-methylotrophs, *Hyphomicrobium*, and *Methylophilaceae*), and process function.

**Conflict of interest** The authors declare that they have no conflict of interest.
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**Figure captions:**

Fig. 1 NO$_x$ reduction, operating conditions, and microbial community dynamics in the denitrification filter of WWTPA (the 10-week follow-up period of microbial communities [27 August 2008 – 28 October 2008] is framed). (a) Temperature and the concentration of NO$_x$ and O$_2$ in the inflow, concentration of NO$_x$ in the outflow, and the relative NO$_x$ reduction. (b) NO$_x$ load in the inflow and outflow, actual NO$_x$ reduction rate, water flow, methanol addition rate, and methanol:NO$_x$ ratio in the inflow. (c) Results of non-metric multidimensional scaling analysis of LH-PCR peak abundance data (1. axis shown, explaining 90 % of the variability in community structure) and relative abundance of methylotrophs, *Hyphomicrobium* (peak 466 bp) and *Methylophilaceae* (peak 521 bp), as well as their sum as a biomarker of methylotrophs and the relative abundance of non-methylotrophs (sum of all peaks except 466 bp, 521 bp and 524 bp) based on the LH-PCR peak data.

Fig. 2 Phylogenetic tree (neighbor joining method) of the 16S rRNA gene clone libraries of the *Hyphomicrobiaceae* assigned operational taxonomic units (OTUs) (at 97 % sequence similarity) in the studied denitrification filters. *Hyphomicrobium* clusters were previously defined by Rainey et al. [30]. The numbers in brackets after the OTU number indicate the number of sequences within that OTU. The numbers at the nodes indicate the percentages of occurrence in 1000 bootstrapped trees (bootstrap values > 50% are shown).

Fig. 3 Phylogenetic tree (neighbor joining method) of the 16S rRNA gene clone libraries of the *Methylophilaceae* assigned OTUs. *Methylophilaceae* clusters were defined in this study (see tree details in the legend of Fig. 2)
Fig. 4 Correlation between the relative abundance of the peaks assigned to (a) *Hyphomicrobium* (peak 466 bp) and *Methylophilaceae* (peak 521 bp) and (b) methylotrophs (sum of 466 bp and 521 bp) and non-methylotrophs (sum of all peaks except 466bp, 521bp, and 524 bp) in the length heterogeneity-PCR (LH-PCR) analysis of WWTPA samples during the 10-week monitoring period. Physicochemical and process variables correlating (p < 0.05) with the relative abundance of both groups in either (a) or (b); the sign of the correlations are shown with black-colored text and dashed-line arrow, whereas those correlating only with one of the groups are shown as gray-colored text and dashed-line arrow.

Online Resource figure captions

Online Resource 1 Operating conditions and functional performance in the denitrification biofilter of WWTPB. (a) Temperature and concentration of NO$_x$ and O$_2$ in the inflow, concentration of NO$_x$ in the outflow, and the relative NO$_x$ reduction. (b) NO$_x$ load in the inflow and outflow, actual NO$_x$ reduction rate, water flow, methanol addition rate, and the methanol:NO$_x$ ratio in the inflow. The date of sampling for microbial studies (2 October 2008) is indicated with an arrow.

Online Resource 2 Hierarchical clustering analysis (UPGMA) of the relative abundance of peaks in the length heterogeneity-PCR (LH-PCR) analysis of the 16S rRNA genes of the inflow water and backwash water of the denitrification biofilters of WWTPA and WWTPB and the carrier material from WWTPB.

Online Resource 3 Electropherograms of the length heterogeneity PCR (LH-PCR) analysis of the 16S rRNA genes in samples of the denitrification biofilters of WWTPA and WWTPB (backwash water from both systems and carrier material from WWTPB) and the inflow water (feed water). The peaks assigned to *Hyphomicrobium* and *Methylophilaceae* at WWTPA are marked by arrows.
Table 1 Characteristics of the municipal wastewater treatment plants (WWTPA and WWTPB) and the studied methanol-fed denitrification biofilters

|                           | WWTPA                        | WWTPB                        |
|---------------------------|------------------------------|------------------------------|
| Type/N removal            | Biol.chem./pre- & postdenitr. | Biol.chem/postdenitr.        |
| Population equivalent     | 740000                       | 31000                        |
| Aver. flow rate (m³/d)    | 280000                       | 14000                        |
| Annual aver. N-reduction (%) | 90                          | 75                           |
| Annual T range (°C)       | 9 - 18                       | 2 - 20                       |
| Number of denitr. filter cells | 10                          | 6                            |
| Bed volume (m³/filter cell) | 432                         | 56                           |
| Carrier material in filter cells | Polystyrene beads  | Polystyrene beads |
| Aver. NO₃⁻ red. (mol/m³/d) | 44                          | 63                           |
| Aver. NO₃⁻ red. (%)       | 89                           | 81                           |
| Aver. surface load (m/h)  | 8.1                          | 3.4                          |
| Aver. hydraulic retent. time (h) | 0.4                        | 0.6                          |

a Annual average relative N-reduction for the whole treatment process in WWTPs

b Average NO₃⁻ reduction expressed per carrier material volume, average relative NO₃⁻ reduction, average surface load, and average hydraulic retention time in the studied filter cell in WWTPA (study period 20 August 2008 – 31 October 2008) and in the whole biofilter system in WWTPB (study period 1 September 2008 – 31 October 2008)
Table 2  Bacterial community composition (% of the 16S rRNA gene sequences) in the
denitrifying biofilters of municipal wastewater treatment plants (WWTPA and WWTPB) based on
clonal library and 454-pyrosequencing analyses of the sheared biomass in backwash water and the
biomass on carrier material (only in WWTPB). Putative methylotrophic taxa are marked with

|                      | WWTPA | WWTPA (454)a | WWTPB | WWTPB.Car (carrier mat.) |
|----------------------|-------|--------------|-------|-------------------------|
| **Number of sequences:** | 45    | 3643         | 58    | 48                      |
| **Frequency (b)**     |       |              |       |                         |
| **Total methylotrophs** | 33    | 28           | 74    | 38                      |
| Alphaproteobacteria  | 7     | 3            | 5     | 15                      |
| Hyphomicrobiaceae     | 7     | 2            | 2     | 10                      |
| *Hyphomicrobium* II  | Meth  | <0.1         | -     | -                       |
| Methylcystaceae       | -     | <0.2         | 3     | -                       |
| Paracoccus            | Meth  | -            | 3     | -                       |
| Bradyrhizobiaceae     | -     | <0.1         | -     | 2                       |
| Bradyrhizobium        | Meth  | -            | -     | 2                       |
| Betaproteobacteria    | 47    | 41           | 74    | 33                      |
| Methylphilaceae       | Meth  | 26           | 25    | 66                      |
| Cluster Met I         | Meth  | -            | -     | 66                      |
| Methylotenera I       | Meth  | 22           | 25    | -                       |
| Methylotenera II      | Meth  | 2            | -     | -                       |
| unclassified          | Meth  | 2            | -     | 2                       |
| Rhodocyclaceae        | 9     | 4            | 3     | 2                       |
| Methylaversatilis     | Meth  | -            | -     | 3                       |
| Comamonadaceae        | 9     | 4            | 2     | 2                       |
| Deltaproteobacteria   | 9     | 10           | 3     | -                       |
| Epsilonproteobacteria | -     | <0.5         | -     | -                       |
| Gammaproteobacteria   | -     | 3            | 2     | 2                       |
| Moraxellaceae         | -     | 1            | -     | -                       |
| Acinetobacter         | Meth  | -            | <0.1 | -                       |
| Methyllococaceae      | Meth  | -            | <0.2 | -                       |
| Acidobacteria         | -     | 1            | -     | 15                      |
| Actinobacteria        | -     | 1            | 2     | 8                       |
| Bacteroidetes         | 9     | 8            | 7     | 6                       |
| Flavobacteriaceae     | -     | 1            | -     | -                       |
| Flavobacterium        | Meth  | -            | 1     | -                       |
| Chloroflexi           | 11    | 2            | 2     | -                       |
| Deinococcus-Thermus   | 2     | <0.1         | -     | 4                       |
| Nitrospirae           | -     | -            | -     | 4                       |
| Planctomycetes        | -     | <0.5         | -     | 8                       |
| unclassified bacteria+others | 15    | 30           | 5     | 5                       |

a Library generated using 454 – pyrosequencing
b Classification was made using RDP database in Mothur and by phylogenetic tree
analysis (Figs. 2 & 3). Assignment to methylotrophic function was based on previous
literature. Frequencies are given as percentages (%) of total number of sequences in a
sample.
c Clustering (clusters I and II) of Hyphomicrobium according to Rainey et al. [30]. See
also Fig. 2.
d Clustering based on Fig. 3.
Figure 1

- **NO\textsubscript{x} in**
- **NO\textsubscript{x} out**
- **relative NO\textsubscript{x} - reduction**
- **O\textsubscript{2} in**
- **Temperature**
Figure 2

Hyphomicrobiurn II

Hyphomicrobiurn I

Filomicrobiurn

Hydrogenovibrio marinus (DB8374)

WWTPA
WWTPB
WWTPB_Car
Figure 3

Methanol-utilizing denitrifying bacteria (in Ginige et al. [10])

Cluster Met I

Methylophilus

Methylobacillus

Methylovorans

OTU 103 (1) (KP098733)

OTU 2 (41) (KP098663)

OTU 117 (1) (KP098692)

OTU 6 (11) (KP098616)

Methylophilaceae (in Ginige et al. [10])

OTU 6 (11) (KP098616)

Methylocutera versatilis (NR 074993)

OTU 112 (1) (KP098795)

OTU 116 (1) (KP098696)

Methylophilaceae 11 (J0KJ01000001)

Methylotenera mobilis (AB661738)

OTU 20 (4) (KP098698)

Methylotenera mobilis 11 (J0KJ01000001)

Methylotenera mobilis 13 (13) (gijJ0E398960:2800-5349)

OTU 137 (1) (KP098672)

OTU 135 (1) (KP098974)

unclassified Methylophilaceae

Methylotenera II

Methylotenera mobilis 7 (731) (gijH0E398960:2800-5349)

Methylotenera mobilis 13 (13) (gijH0E398960:2800-5349)

Methylphilage marina (X87338)
Figure 4

![Graph a](image)

**Graph a:**
- **Increasing** actual NO$_3^-$ reduction rate
- **Increasing** N load (NO$_3^-$ + CH$_4$ addition (Me) and water flux (Wf))
- $r^2 = 0.83$, $p < 0.001$

**Graph b:**
- **Increasing actual NO$_3^-$ reduction rate
- **Increasing** N load (NO$_3^-$ + CH$_4$ addition (Me) and water flux (Wf))
- $r^2 = 0.94$, $p < 0.001$

**Methylophilaceae (521 bp) (%)**
**Hyphomicrobiurn (466 bp) (%)**
**Non-methylotrophs (%)**
**Increasing temperature (T)**

**Total methylotrophs (521bp + 466bp) (%)**
**Increasing temperature (T)**
Online Resources (1-3)

Journal: J Ind Microbiol Biotechnol

Title: Methylophilaceae and Hyphomicrobium as target taxonomic groups in monitoring the function of methanol-fed denitrification biofilters in municipal wastewater treatment plants

Authors: Antti J. Rissanen1,2,*, Anne Ojala, Tommi Fred, Jyrki Toivonen & Marja Tiirola

1Department of Chemistry and Bioengineering, Tampere University of Technology, P.O. Box 541, FI-33101 Tampere, Finland
2Department of Biological and Environmental Science, University of Jyväskylä, P.O. Box 35, FI-40014 University of Jyväskylä, Finland

*Corresponding author
e-mail-address: antti.rissanen@tut.fi
Operating conditions and functional performance in the denitrification biofilter of WWTPB. (a) Temperature and concentration of NO\textsubscript{x} and O\textsubscript{2} in the inflow, concentration of NO\textsubscript{x} in the outflow, and the relative NO\textsubscript{x} reduction. (b) NO\textsubscript{x} load in the inflow and outflow, actual NO\textsubscript{x} reduction rate, water flow, methanol addition rate, and the methanol:NO\textsubscript{x} ratio in the inflow. The date of sampling for microbial studies (2 October 2008) is indicated with an arrow.
Hierarchical clustering analysis (UPGMA) of the relative abundance of peaks in the length heterogeneity-PCR (LH-PCR) analysis of the 16S rRNA genes of the inflow water and backwash water of the denitrification biofilters of WWTPA and WWTPB and the carrier material from WWTPB
Online Resource 3

Electropherograms of the length heterogeneity PCR (LH-PCR) analysis of the 16S rRNA genes in samples of the denitrification biofilters of WWTPA and WWTPB (backwash water from both systems and carrier material from WWTPB) and the inflow water (feed water).

The peaks assigned to *Hyphomicrobium* and *Methylophilaceae* at WWTPA are marked by arrows.