

Bacterial changes in a full-scale drinking water distribution system after the removal of monochloramine



Conclusions

- Removing monochloramine (MCA) did not jeopardize drinking water quality.
- The microbial community changed after removal of MCA; the %HNA (high nucleic acid) bacteria decreased from 55 – 90 % to 45 – 60 %; and TCC (total cell count) increased at points that had been previously exposed to MCA.
- Customized data analysis tools enabled a fast analyse of the large FCM data set with visualization of the microbial changes, showing that a bacterial community that used to differ largely became more homogenous.

Introduction

- Flow cytometry (FCM) is a useful technology for monitoring of microbiological changes in water but produces big data sets
- In January 2020, the water treatment plant (WTP) Kvarnagården in Varberg, Sweden, removed the disinfectant MCA after two years of establishing FCM baselines along the entire drinking water distribution system (DWDS)
- Fast and efficient data handling was necessary to detect if and where changes in the microbiological community occurred

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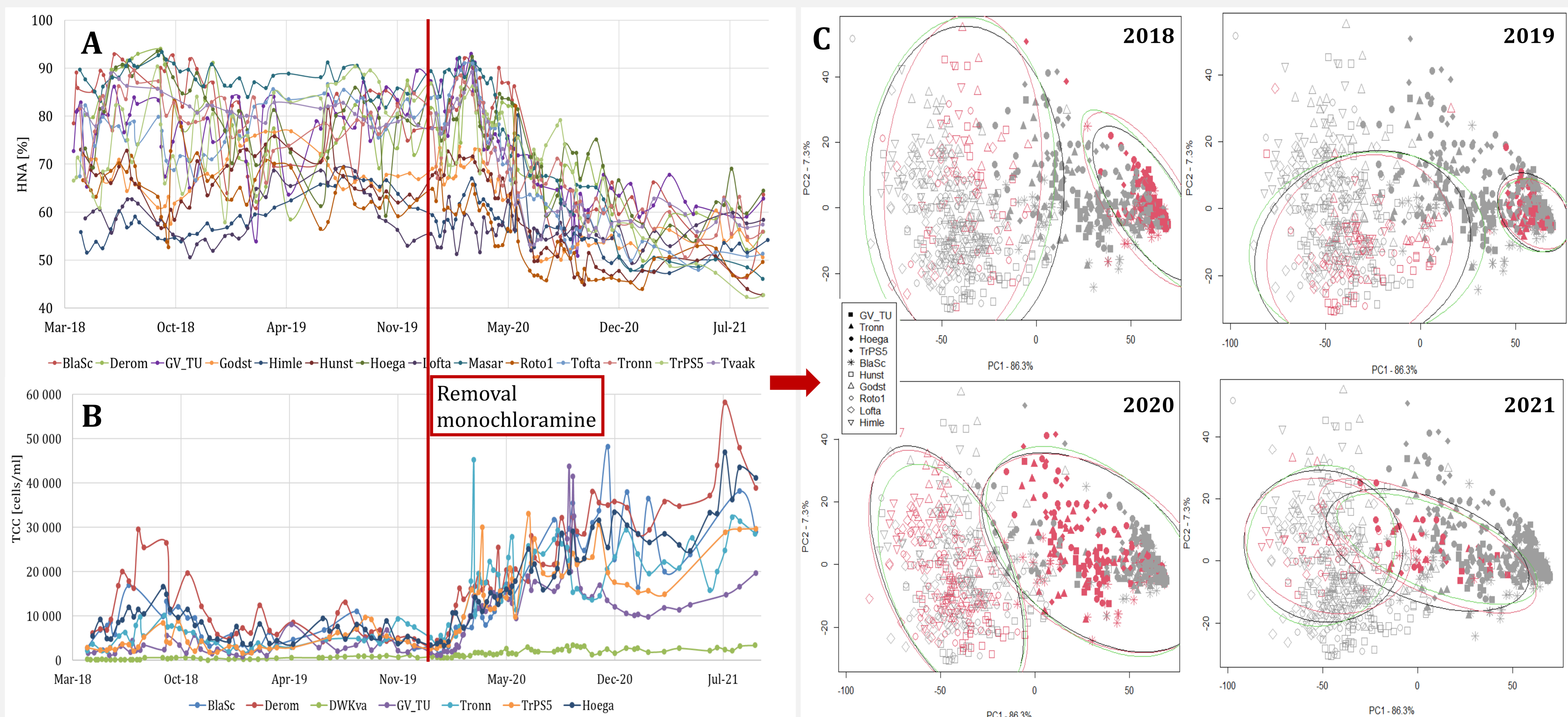


Figure 1: Comparison of bacterial populations between 2018-2021, before and after removal of MCA in a DWDS. A: %HNA of bacteria in the DWDS. B: Comparison of TCC (cells/ml) at points that have been exposed to MCA before the removal. C: PCA plots showing bacterial changes in the water phase after the removal of MCA at 10 points in the DWDS using FCM fingerprints. Five points were exposed to MCA before the removal (GV_TU, Tronn, Hoega, TrPS5, BlaSc) and five points had not been exposed (Hunst, Godst, Roto1, Lofta, Himle). The plots show all data points (grey) with red highlighting the data points for respective years. A clear shift of the sampling points that have been exposed to MCA prior removal towards those that have not been exposed is visible, leading to a merge of both clusters.

Method

- FCM analysis from 16 locations in the DWDS + WTP over 3.5 years
- data analysis with custom scripts in R based on FCM fingerprints
- Principal component analysis (PCA) with bootstrap ellipses to fit a 2D gaussian probability distribution with 95 % confidence area

Results

- Changes in bacterial community were observed after removal of MCA
- Percentages of HNA bacteria decreased at all sampling points, from 55 – 90 % to 45 – 60 % (Figure 1A)
- TCC increased in parts of the DWDS that had been exposed to MCA before the removal (Figure 1B)
- Bacterial community at DWDS locations that used to differ largely regarding TCC and %HNA became more homogenous after removal of MCA with calculated separation between clusters decreasing to almost zero (Figure 1C)