

Microbial Ecology of Drinking Water Distribution Systems - A Study

Dr. Kamini Sharma,
Department of Chemistry,
Jodhpur Institute of Engineering and Technology
Jodhpur-Rajasthan, India

Abstract:- Available scientific literature fuelled by the application of recent advances in molecular-based methods to drinking water ecosystem indicates that drinking water distribution Systems (DWDS) are of diverse microbial ecosystems, with high bacterial and fungal abundance, but where a variety of microbial life from viruses to protozoa can be found. Treated water is transported to end users through a diverse and complex water distribution infrastructure. Preventive measures are taken to control water quality, including microbial contamination.

Once microorganisms are within a DWDS they will face a challenging environment, with limited nutrients and changing water flow and pressure fluctuations. As a consequence, microorganisms will often have a better chance of survival attached to the pipe surfaces within a biofilm.

This review presents an overview of the available methods that can be used to detect microorganisms and assess their abundance, composition and function within drinking water distribution Systems.

SAMPLING WATER DISTRIBUTION SYSTEMS

Currently two different approaches exist for studying biofilms in situ in drinking water distribution Systems. One involves cut-outs of pipes; the other one relies on devices inserted into the pipe.

Conventional and current microbiological techniques *Culture-dependent techniques*

The reference method used for routine bacteriological monitoring in drinking water is heterotrophic plate count (HPC) measurements, which assess only heterotrophic bacteria able to form colonies on a solid medium at a specific temperature. Counting the number of colonies grown after a defined incubation time provides a general estimation of the bacteriological load in the water samples. There are several standardized HPC methods. Culture-dependent tests are also used to detect indicator microorganisms such as coliform bacteria. The membrane filtration (MF) technique and the multiple tube fermentation (MTF) method are often used to detect coliforms in drinking water.

MICROSCOPY METHODS.

Epifluorescence microscopy based methods offer a faster alternative for monitoring the quality of drinking water than traditional plate counts,

Which have long incubation times. Different fluorescent dyes can be used to directly stain cells in biofilms or water samples and to estimate total cell counts using an

epifluorescence microscope. Fluorescent in situ hybridization (FISH) effectively extends epifluorescence microscopy, allowing for the fast detection and enumeration of specific microorganisms. This method uses fluorescent labelled oligonucleotide probes which bind specifically to microbial DNA in the sample, allowing the visualization of the cells using an epifluorescence or confocal laser scanning microscope (CLSM). An alternative fast and reliable method to monitor bacterial abundance and viability of planktonic cells or cells in suspensions is flow cytometry (FC).

PCR BASED METHODS.

The polymerase chain reaction (PCR) is a method used to amplify (i.e. obtain multiple copies) fragments of DNA. The most useful PCR-based techniques to detect microorganisms in drinking water are multiplex PCR and quantitative real time (qPCR). Multiplex-PCR uses several oligonucleotide probes to simultaneously detect different microorganisms and has been used in drinking water related research to detect faecal indicators or pathogens. q-PCR is a sensitive tool to detect and quantify microorganisms in environmental samples based on quantifying the number of target gene copies present in a sample.

MICROBIAL COMMUNITY COMPOSITION

This information is essential in order to detect pathogens, microorganisms associated with corrosion or water discoloration, to monitor biofilm formation on pipes, to assess the influence of abiotic factors on microbial communities and to compare diversity between different

Molecular techniques

Molecular analysis of samples includes the extraction and purification of DNA or RNA. DNA provides information of the total microbial community of the samples while RNA-based analysis represents only the active part. The nucleic acid extraction is followed by PCR amplification of "marker genes" to obtain taxonomic information

Estimation of biomass

Two methods widely used in drinking water research to estimate biomass and bacterial growth are the quantification of adenosine triphosphate (ATP) and of assimilable organic carbon (AOC) respectively.

Proteomics is a discipline focused on the identification of proteins and metaproteomics can be defined as the characterisation of the entire protein complement of a

microbial community . Protein expression can be directly associated with specific microbial activities.

Microautoradiography (MAR) is a radioactive approach used in combination with FISH to reveal the physiological properties of microorganisms with single-cell resolution . MAR-FISH provides information on total cells, probe targeted cells and the percentage of cells that incorporate a given radiolabelled substance . This method has been widely applied to study the structure and function of microbes in freshwater and marine ecosystems including biofilms

QUORUM SENSING

The biochemical process of cell to cell communication is known as quorum sensing (QS) and it plays an important role in initial cell attachment to surfaces and in the control of biofilm growth.

REFERENCES

- [1] Szewzyk, U., Szewzyk, R., Manz, W., Schleifer, K.H., 2000. Microbiological safety of drinking water. *Annu Rev. Microb.* 54,81-127.
- [2] Henne, K., Kahlisch, L., Brettar, I., H€ofle, M.G., 2012. Analysis of structure and composition of bacterial core communities in mature drinking water biofilms and bulk water of a citywide network in Germany. *Appl. Environ. Microb.* 78, 3530-3538.
- [3] Kahlisch, L., Henne, K., Gr€ofe, L., Brettar, I., H€ofle, M., 2012. Assessing the viability of bacterial species in drinking water by combined cellular and molecular analyses. *Microb. Ecol.* 63,383-397.
- [4] Wilmes, P., Bond, P.L., 2006. Metaproteomics: studying functional gene expression in microbial ecosystems. *Trends Microb.* 14,
- [5] Gilbride, K.A., Lee, D.Y., Beaudette, L.A., 2006. Molecular techniques in wastewater: understanding microbial communities, detecting pathogens, and real-time process control. *J. Microb. Method* 66, 1-20.
- [6] Bej, A.K., McCarty, S.C., Atlas, R.M., 1991. Detection of coliform bacteria and *Escherichia coli* by multiplex polymerase chain reaction: comparison with defined substrate and plating methods for water quality monitoring. *Appl. Environ. Microb* 57, 2429-2432.
- [7] Guy, R.A., Payment, P., Krull, U.J., Horgen, P.A., 2003. Real-Time PCR for quantification of *Giardia* and *Cryptosporidium* in environmental water samples and sewage. *Appl. Environ. Microb.* 69, 5178-5185.
- [8] LeChevallier, M.W., Liu, W.-T., 2010. Pyrosequencing analysis of bacterial biofilm communities in water meters of a drinking water distribution system. *Appl. Environ. Microb.* 76,5631-5635
- [9] Martiny, A.C., Jørgensen, T.M., Albrechtsen, H.-J., Arvin, E., Molin, S., 2003. Long-term succession of structure and diversity of a biofilm formed in a model drinking water distribution system. *Appl. Environ. Microb.* 69, 6899-6907.
- [10] Ramalingam, B., Sekar, R., Boxall, J., Biggs, C., 2013. Aggregation and biofilm formation of bacteria isolated from domestic drinking water. *Water Sci. Technol. Water Supply Raunkjaer, K., Hvitved-Jacobsen, T., Nielsen, P., 1994.*