Drinking water quality assessment using Next-Generation Sequencing of bacterial DNA and RNA

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Motivation

Water source, treatment scheme and distribution are three factors that influence the water microbial community and their metabolic activities[1,2]. After producing drinking water at the treatment plant, the microbial community is influenced by the materials of the distribution system, residence time, temperature shifts, flow pattern variations, pressure changes and presence of chemical compounds.

Next-Generation Sequencing (NGS) techniques can be employed to gain insights into the microbial community composition of a water sample as well as the respective metabolic activity. This provides detailed information in a short time. Information obtained can be the deoxyribonucleic acid (DNA) or the ribonucleic acid (RNA) content of organisms present. DNA sequences enable characterization of the microbial population as well as the metabolic potential. RNA sequences give information on the metabolic state of the microbial community.

In this project we will investigate whether the microbial drinking water population, determined using NGS technology, can be used to infer chemical water quality (Fig.1).

Technological challenge

To use the microbial community as a water quality indicator, the initial challenge will be to integrate DNA and RNA data sets in order to understand the metabolic potential and the actual activity of the existing microbial population. Correlating these results in a meaningful way to chemical water quality will be the most important step in the analysis. The final task is to identify key microbial response patterns that can be reliably identified as "fingerprints" describing microbial and chemical drinking water quality.

Analyses of NGS data will be performed using existing bioinformatics tools and statistical methods. The tools will be extended and optimized in order to handle these large NGS data sets in a short time. New software tools predicting the presence of xenobiotics, toxic compounds or critical metabolic by-products in water will be developed.

[1] Roeselers, G. et al., Environmental Microbiology (2015) Microbial biogeography of drinking water: patterns in phylogenetic diversity across space and time.
[2] Pinto, A. J. et al., Environmental Science & Technology (2012) Bacterial community structure in the drinking water microbiome is governed by filtration processes.
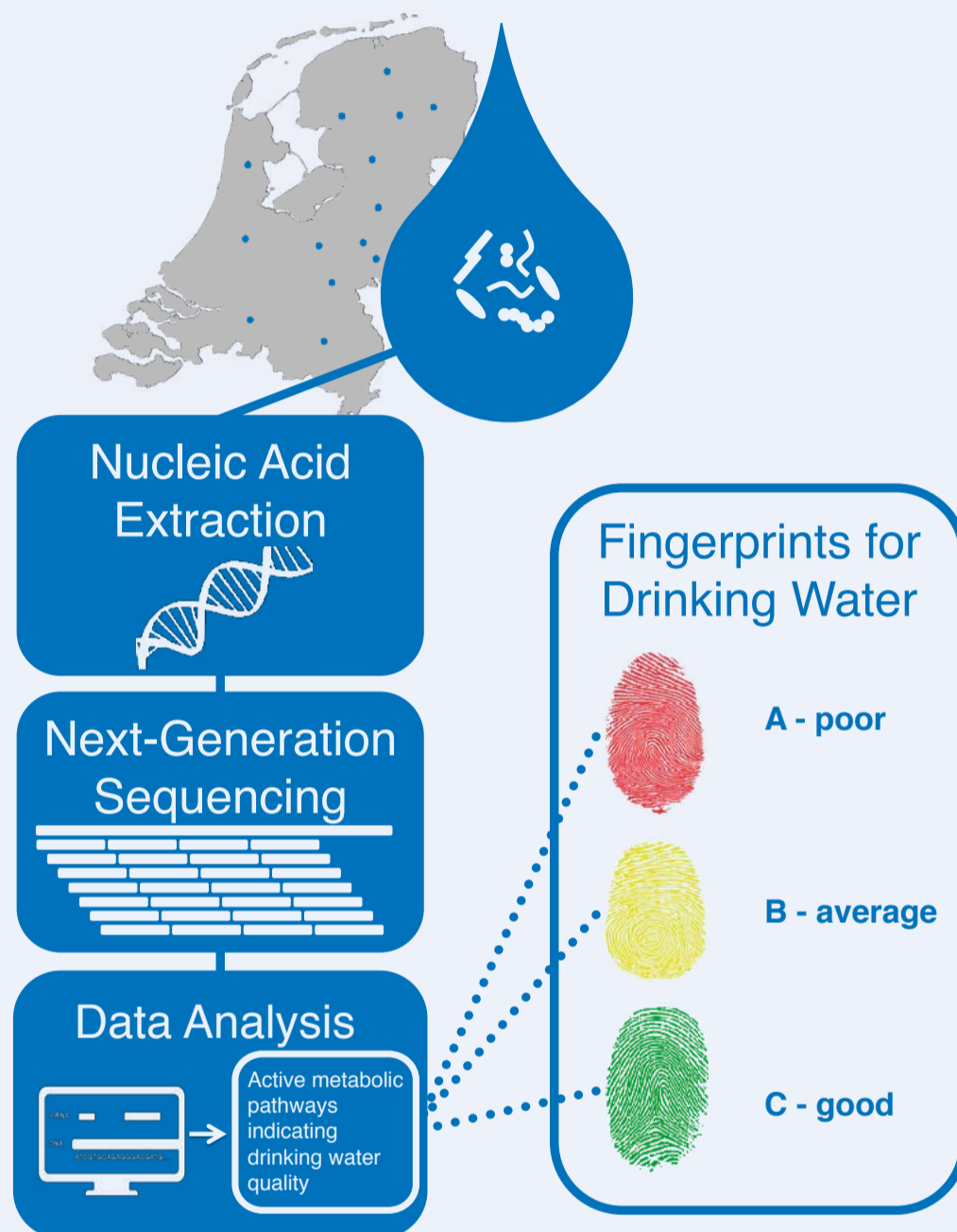
Fig.1 Top left: Map of the Netherlands and potential water source sampling points (blue dots). Samples are represented by the droplet. The analysis workflow on samples consists of nucleic acid extraction, NGS and data analysis. Data analysis results lead to characteristic fingerprints that can indicate (A) poor, (B) average or (C) good microbial and chemical water quality.

Research goals

- Detect changes in microbial communities and their metabolic activities using NGS technology throughout the drinking water distribution system over time.
- Record comprehensive data sets (from source to tap) that enable to correlate distribution system parameters (e.g. temperature, materials etc.) in relation to chemical (e.g. xenobiotics) and microbiological water quality.
- Identify "fingerprints", in other words: characteristic genomic and transcriptomic signatures, which can be used to quickly obtain information about water quality.

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