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## Technical Note: Community of bacteria attached on the PVDF MF membrane surface fouled from drinking water treatment, in Seoul, Korea

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**Abstract.** Alpha, beta, and gamma proteobacteria comprise approximately 68, 16, and 7% of all identified bacteria. In this study, bacterial communities that had fouled polyvinylidene fluoride microfiltration membranes, which are used for drinking water treatment, over an 18 month period were analyzed using the 16s rRNA gene clone library method. The alpha, beta, and gamma proteobacteria were composed of mainly *Bradyrhizobium* and *Rhodopseudomonas*, *Ralstonia*, and *Legionella*, respectively. The presence of a relatively high amount of alpha proteobacteria was due to the oligotrophic condition of the drinking water source, the Han River, tested in this specific case study. The second most prominent bacteria community was the beta proteobacteria, which are typically found in a freshwater environment. This finding supports the notion that the drinking water source was relatively clean. Analyses of the organic foulants indicated that they were most likely from extra cellular polymers and/or cell fractured chemicals from bacteria or micro-organisms, as identified using organic characterizing tools, including 3-D fluorescence excitation-emission matrix and Fourier transform IR analyses.

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