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Groundwater Flow Process and Microbial Dynamics in a Mountainous Forested Catchment

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The groundwater contains a lot of microbes, which those communities are related to the surrounding environment of them. However, the relationship between groundwater flow process and microbial community constituents and abundance has not been investigated enough.

In this study, we investigated the spatiotemporal variation of the microbial community in the spring water and groundwater to reveal the relationship between the groundwater flow system and microbial communities. We performed an intensive water sampling and monitoring in a mountainous forested catchment in Kawamata Town, Fukushima Prefecture, Japan, where basic hydrological data are available. We monitored seven piezometers and two springs on the hillslope and the valley bottom. Throughout the sampling, monitoring and analysis, we obtained the microbial information such as the density of prokaryotes by total direct counting (TDC), community constituents revealed by the next generation sequencing (NGS) method and the microbial diversity in addition to the physicochemical parameters, general water quality and mean residence time of groundwater using sulfur-hexafluoride (SF_6).

The mean residence time of the spring water and groundwater ranged from less than 1 year to 30 years. The density of prokaryotes ranged from 5.37×10^3 cells/mL to 2.01×10^6 cells/mL (n=60). The most abundant prokaryotes shown by NGS were *Proteobacteria* or *Acidobacteria*, suggesting that the environment surrounding those microbes was aerobic subsurface. The analysis of the diversity shows that the species richness is the highest in the spring water, and analysis of the community similarity suggests that the communities relate with the groundwater table fluctuation. Thus, these show that the environmental microbial dynamics in the groundwater reflect not only the surrounding environment but also the groundwater flow itself.