

Community structures and activity of denitrifying microbes in forested catchment: survey using nitrite reductase genes

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To elucidate the mechanisms of denitrification processes in the forested catchment, microbial ecological approaches have been applied in an experimental watershed that has previously investigated its hydrological processes. The study catchment is located in the Chiba prefecture in central Japan under the temperate Asian monsoon climate. Potential activities of denitrification of soil samples were measured by incubation experiments under anoxic condition associated with $\text{Na}^{15}\text{NO}_3$ addition. Existence and variety of microbes having nitrite reductase genes were investigated by PCR amplification, cloning and sequencings of nirK and nirS fragments after DNA extraction. Contrary to our early expectation that the potential denitrification activity was higher at deeper soil horizon with consistent groundwater residence than that in the surface soil, denitrification potential was higher in shallower soil horizons than deeper soils. This suggested that the deficiency of NO_3^- as a respiratory substrate for denitrifier occurred in deeper soils especially in the summer. However, high denitrification activity and presence of microbes having nirK and nirS in surface soils usually under aerobic condition was explainable by the fact that the majority of denitrifying bacteria have been recognized as a facultative anaerobic bacterium. This also suggests the possibility of that denitrification occurs even in the surface soils if the wet condition is provided by rainwater during and after a storm event. Community structures of microbes having nirK were different between near surface and deeper soil horizons, and ones having nirS was different between saturated zone (under groundwater table) and unsaturated soil horizons. These imply that microbial communities with nirK are sensitive to the concentration of soil organic matters and ones with nirS is sensitive to soil moisture contents.

Keywords: forest soil, denitrification, microbial community, functional gene