

Assessing the Impact of Agriculture on the Diversity of Groundwater Microbial Communities in Nueva Ecija, Philippines

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ABSTRACT

Groundwater is a critical resource for agricultural areas, however, intensive fertilizer application has heightened concerns on mobilization and leaching of agrochemicals into groundwater systems. This may alter groundwater quality and the living systems such as microbial communities that inhabit these subsurface environments. These groundwater microorganisms play an essential role in mediating biogeochemical processes, and contributing to water quality maintenance and ecosystem functioning. Consequently, changes in the composition of groundwater microbial communities may affect the ecosystem and the services it provides.

Amplicon sequencing was employed to assess the influence of agricultural land-use on the diversity and function of groundwater microbial communities in selected sites in Nueva Ecija, Philippines. Results showed that pH, oxidation-reduction potential, electrical conductivity, salinity, total dissolved solids, and nitrate concentrations of agricultural sites were significantly different from pristine groundwater. Taxonomic profiling showed agricultural sites are dominated by *Bacillaceae*, *Rhodocyclaceae*, and *Gallionellaceae*, whereas *Desulfovibrionaceae* and *Sphingomonadaceae* were most abundant in pristine groundwater. Archaeal communities also showed higher abundance of Halobacteriota, Nanoarchaeota, and Micrarchaeota in agricultural sites, while pristine sites

were dominated by Methanobacteriota. Diversity analyses revealed microbial community composition shifted significantly, while alpha diversity remained unchanged. Moreover, microbial communities in pristine groundwater were found to be abundant in genes coding for nutrient acquisition and anaerobic energy metabolism, while agricultural groundwater had greater abundance of genes involved in nutrient assimilation and processing, consistent with elevated nutrient availability. Lastly, ordination and correlation analyses revealed that ORP are influencing community turnover, while phosphates are the significant driver of alpha diversity.

This study demonstrated that agricultural land-use in Nueva Ecija influences the groundwater physicochemical parameters, affecting the structure and inferred functional potential of microbial communities. A baseline taxonomic and functional profile for the pristine and agricultural groundwater in Nueva Ecija was also established which may be useful for future studies. Ultimately, this work has shown that microbial community profiling provides robust and biologically-grounded assessment of groundwater quality.

Keywords: *groundwater, agriculture, 16S rRNA amplicon sequencing, microbial communities, taxonomic profile, functional profile*