

# **Microbial Community Profiling of Groundwater within Agricultural Areas in Nueva Ecija, Philippines using Shotgun Metagenomic Sequencing**

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## **Abstract**

Groundwater ecosystems provide multitudes of benefits that are essential to the maintenance of human life. However, the advent of modern production-oriented agriculture has prompted the use of high amounts of agrochemicals which threatened the health status of many natural groundwater reserves. Traditional monitoring of groundwater ecosystems is done through water quality assessments and profiling of macroinvertebrates. These techniques, however, are slow, laborious, and only show a small portion of the true diversity and status of groundwater ecosystems. Notably, groundwater microbial communities are the unseen majority, which drives the key biogeochemical cycle and should also be included in routine groundwater assessments. However, information about microbial profiles is still limited by their unculturable status. Furthermore, the impact of agrochemicals on groundwater microbes remains to be largely unexplored, especially in many agricultural areas in the Philippines. Hence, with the use of shotgun metagenomic sequencing, the present study aims to determine the impact of agriculture on the diversity and function of groundwater microbial communities within agricultural areas in Nueva Ecija, Philippines. To address this purpose, the specific objectives of the study are to (1) describe and compare the taxonomic and functional profiles of the microbial communities in the groundwater within agricultural and pristine areas; (2) determine the ecological diversity of the identified microbial communities in the selected groundwater study sites; and, (3) determine key environmental factors shaping the microbial communities in the agricultural and pristine groundwater. The study will provide baseline data for groundwater microbial diversity as an indicator of groundwater health within agricultural areas in the Philippines.

*Keywords:* groundwater, metagenomics, microbial community, agriculture