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COMPARISON OF THE FUNGAL PROFILE OF AQUACULTURE AND NON-AQUACULTURE WATER IN TAAL LAKE, BATANGAS, PHILIPPINES THROUGH PCR-DGGE OF THE 18S rRNA GENE

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ABSTRACT – Profiling of fungal communities is now an emerging tool for assessing the effects of stress in aquatic ecosystems. In the present study, we determined if there is a difference in fungal community structure in the Taal Lake ecosystem as a result of intensive aquaculture activities. Fungal profiles of aquaculture (Bañaga area) versus non-aquaculture waters (Gonzales area) along Taal Lake were obtained through PCR-DGGE of the 18S rRNA gene. Three indices were determined by DGGE band analysis using Bio-Rad QuantityOne™ software. Dice's Similarity Coefficient was used to determine similarity. Both the Shannon and Simpson indices were generated to compare the diversity of the two sites. The Dice's Similarity Coefficients between the two sites were low, with a mean value of 39.58. Mean values among aquaculture samples (36.74) and non-aquaculture samples (41.83) were also low, suggesting difference in species composition were present in sample replicates. The values of Shannon Diversity (2.73 vs 2.67) and Shannon Evenness (0.87 vs 0.85) indices suggest a more diverse non-aquaculture fungal community compared to the aquaculture community. Cultural and morphological characterization revealed culturable fungal species, such as *Aspergillus niger, A. terreus* and *Penicillium* sp. Sequencing of distinct DGGE bands also revealed the presence of several unknown and uncultured fungal species.

Keywords: fungi, aquaculture, PCR-DGGE, Taal Lake. Dice similarity index, diversity indices

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