## MICROBIAL COMMUNITY ANALYSIS OF ANAMMOX IN FILTER BIOREACTOR (FtBR)

## FINAL PROJECT

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## ABSTRACT

Nitrogen pollution represents a considerable environmental threat to aquatic ecosystems, thereby necessitating the development of innovative wastewater treatment technologies. This study investigates the microbial community structure within a Filter Bioreactor (FtBR) for nitrogen removal through anaerobic ammonium oxidation (Anammox) in saline wastewater. The FtBR, as conducted by Indira, 2024, was inoculated with sludge from Vaname shrimp ponds (Katapiang, Padang Pariaman) and fed artificial seawater-based wastewater containing 70 mg-N/L of ammonium and nitrite. It was operated for 175 days at 25-28 °C and 30.1-33.0 parts per thousand (ppt) salinity. Microbial communities in the biomass samples (day 0 and 132) were analyzed after completing the FtBR operation through 16S rRNA gene sequencing (NGS, MiSeq Illumina). The predominant phyla identified were Proteobacteria (27.14%), Chloroflexi (17.59%), and Planctomycetota (14.75%). The most abundant genera included Candidatus Brocadia (8.07%), Marinobacter (3.18%), and EBM-39 (2.92%). Two Anammox genera, namely *Candidatus Brocadia* and *Candidatus Jettenia* (which includes four associated species), were identified; however, *Candidatus Scalindua*, recognized as a marine anammox bacterium, was not detected. Their co-occurrence with ammonia-oxidizing bacteria (AOB), nitrite-oxidizing bacteria (NOB), and other supportive microbes suggests complex ecological interactions. These findings significantly enhance the understanding of the microbial community structure within the FtBR, providing crucial insights into the key microorganisms that are active in saline Anammox systems.

**Keywords:** Anammox, filter bioreactor, nitrogen removal, microbial community, 16S rRNA gene sequencing

