CHAPTER V

CONCLUSION AND SUGGESTION

5.1 Conclusion

Based on the results and discussion of research on the anammox bacterial community in the filter bioreactor (FtBR), it can be concluded that:

1. The Filter Bioreactor (FtBR) shows a microbial community increasing in *Planctomycetota* at 14.75% and *Chloroflexi* at 17.59%. Meanwhile, *Bacteroidota* decreased to 2.31%, and in contrast, genera in the inoculum, such as *Robiginitalea* at 4.39%, have reduced abundance;
2. Anammox bacteria were enriched in the FtBR, reaching 8.95% relative abundance. Phylogenetic analysis confirmed that the community primarily comprised *Candidatus Brocadia* (8.07%) and *Candidatus Jettenia* (0.88%), with four species. The marine anammox genus *Candidatus Scalindua* was not detected;
3. Key microbial groups played distinct roles in FtBR's nitrogen removal. Anammox bacteria (*Candidatus Brocadia* and *Candidatus Jettenia*) were primary nitrogen removers, Ammonia Oxidizing Bacteria (AOB), such as *Nitrosomonas* (0.80%), partially nitrify by oxidizing ammonium to nitrite, providing a substrate for anammox. Nitrite Oxidizing Bacteria (NOB), specifically *Nitrospira* (0.32%), exhibited suppressed activity, favorable for maximizing N_2 removal via an anammox pathway.

5.2 Suggestion

Based on the research that has been done, some things that can be done for further research are:

1. Always monitor reactor performance to minimize inhibition and conduct experiments in conjunction with microorganism monitoring.
2. For further operation of FtBR using inoculum from marine sediments to obtain marine anammox bacteria
3. Metagenomic research is needed to confirm the presence of new species;

4. The biomass must be sampled at various times and conditions to obtain the microbial community dynamics.