

where none of the p-values generated from the linear models were below 0.05.

3.5 Analysis of results from Mothur and QIIME2 processed data

We observe no significant differences between the Mothur and QIIME2 data in terms of depths, oxygen concentration, and richness. However, there were some differences that should be noted:

- 1) Higher Shannon's Diversity Index was noted in QIIME2 vs. Mothur in terms of oxygen concentrations and anoxic versus oxic levels (Fig. 1 and 2).
- 2) More phyla observed from Mothur (18) than QIIME2 (10) (Table 1).
- 3) An extra genus was present in the genus distribution of the Planctomycetes phylum across samples from Mothur: *Pla3_lineage_ge* (Fig. 5).
- 4) In terms of abundance, the genus distribution of *Planctomyces* in QIIME2 data was higher than Mothur (Fig. 5).
- 5) The scaling of abundance (Fig. 5) in the genus distribution of Planctomycetes across samples from Mothur were also noted to be higher than the scaling of QIIME2 data (Mothur has the Saanich depth of 165m to be approx. 2.0 for abundance whereas QIIME2 has the Saanich depth of 165m to be approx. 1.2 for abundance).

4 Discussion

Planctomyces, also known as anammox bacteria, are known to perform an important process in the nitrogen cycle: Anammox ($\text{NO}_2^- + \text{NH}_4^+ \rightarrow \text{N}_2 + 2\text{H}_2\text{O}$). Anammox can be carried out under anaerobic conditions and is an important process for recycling nitrogen back into the environment and for waste-water treatment [19].

One study have suggested that approximately 30–50% of the total nitrogen loss is currently estimated to take place in OMZs (Oxygen Minimum Zone), and very low concentrations of ammonium in suboxic waters indicate that the anammox process could play an important role in these ecosystems [19]; it was reported that anammox bacteria were very sensitive to oxygen and that oxygen concentrations as little as $1\mu\text{M}$ can reversibly inhibited the anammox reaction. It has also been suggested that the ammonium concentrations were below the detection limit in OMZs and anammox, rather than heterotrophic denitrification, was responsible for the nitrogen loss [19]. Since anammox bacteria abundance was correlated with nitrogen loss, it was expected that there will be higher levels of anammox bacteria such as *Planctomyces* in OMZs. Therefore, based on the information provided by the study, the fact that no relationship is observed between the abundance of *Planctomyces* with oxygen level and ocean depth is not expected.

However, another study had pointed out that *Planctomyces* were most abundant in the oxic part of the wetland profiles [20]. The respective cell numbers were in the range $1.1 - 6.7 \times 10^7$ cells g^{-1} of wet peat, comprising 2 – 14% of total bacterial cells, and displaying linear correlation to the peat water pH [20]. This result contradicted with the research study done by Koo et al. [19], which observed the decline of *Planctomycetes* population at the oxic part of the ocean [19]. Also, Dedysh and Ivanova suggested that different species of Planctomycetes colonized different parts of the ocean: Oxic peat layers were dominated by representatives of the Isosphaera-Singulisphaera