CHAPTER 6.0: CONCLUSION

All soil and sediment samples collected from eighteen sites around Dasan Station, Ny-Ålesund, Norway were varied in pH and salinity (electrical conductivity). The marine, beach, melt lake, and inland lake bank samples studied were alkaline while the terrestrial and periglacier samples were found in a range from slightly acidic to alkaline pH.

The bacterial diversity was significantly correlated (P = 0.001) with samples pH (r = 0.470) and conductivity (r = 0.294). Higher prevalence of *Bacteroidetes* in marine (22.45%) and beach (28.57%) samples that have moderate alkaline environment compared to other samples studied (<21.05%) that have slightly acidic to alkaline condition, indicating *Bacteroidetes* were more prevalent in alkaline samples.

The yield of genomic DNA extracts from Arctic soils and sediments varied between the samples, with higher protein and humic acid content indicating higher input of plants, human activities, and animal droppings into the samples. However, marine samples have less protein content compared to that of samples from other studied sites, probably due to the low input of animal droppings in marine samples, as compared to that of land samples.

In this study, the presence of humic acid in genomic DNA extracts was reduced with a 10-fold dilution of DNA template in PCR and resulting in a clearer DGGE banding pattern. The nonspecific bindings of primary products and DNA smear that were observed in secondary PCR, due to the inhibitors (high humic acid content) in samples did not have any significant influences on the DGGE banding patterns.

nMDS plots and Hierarchical cluster analysis showed all samples were eventually clustered into two groups: marine and non-marine samples. Furthermore, a trend of diversity overlap between samples from close vicinity was observed. This perhaps highlighted the effect of local environmental influences to the soil bacterial composition.

From all eighteen studied sites, soil from the tundra site (sample 17) appeared to have the most diverse bacterial community structure (H' = 2.639). While inland lake bank sediment from the freshwater site (sample 35) showed the least diverse bacterial community structure (H' = 1.792). In contrast, the bacterial diversity of marine samples seems to be varied according to the sample depth, where higher bacterial diversity was found in shallower sediments (sample 24) as opposed to the deeper sediments (sample 30). H' value inferred directly from the DGGE binary data might not reflect the true diversity in the soils and sediments studied. Nevertheless, H' was used here to allow a coarse comparison of "diversity richness" between samples studied. Apparently, H' seems a good general measure to use with diverse community samples.

Out of 28 DGGE bands that were sequenced, four sequences each were related to *Bacteroidetes* and *β-proteobacteria*, two each were related to *Cyanobacteria*, *Firmicutes* and *Fusobacteria*, and one each were related to *Acidobacteria*, *ε-proteobacteria*, *δ-proteobacteria*, *Fibrobacteres* and *Nitrospira*. *Bacteroidetes* were dominant in marine (22.45%) and beach samples (28.55 %) while *β-proteobacteria* were the dominant group in terrestrial (15.85 %) and melt lake (21.05 %) samples. The inland lake bank samples were dominated (14.81 %) by *Cyanobacteria*, *Fibrobacteres*, *Firmicutes* and *Betaproteobacteria*. Where as, the periglacier samples were dominated (21.05 %) by *Bacteroidetes* and *Betaproteobacteria*.

Phylogenetic analysis of sequences of well-defined DGGE bands displayed four distinct clades, which consisted of (i) *Bacteroidetes* and *Cyanobacteria*; (ii) *Firmicutes*, *Nitrospira*, *Fibrobacteres*, *Acidobacteria*, *ε-proteobacteria* and *δ-proteobacteria*; (iii) *β-proteobacteria*; and (iv) *Fusobacteria*. Results showed *β-proteobacteria* (available only in non-marine samples) were not closely related with *δ-proteobacteria* and *ε-proteobacteria* (available only in marine samples), indicating their distinct role in the distinct environment.

There was a distinct clade of uncultured representatives that were not closely related to any known GenBank sequences, this probably represent a potential gene pool of new species. So, a combination of conventional culture-dependent and culture-independent molecular approach that could provide better understanding is suggested for future studies.