CHAPTER 1.0: INTRODUCTION

Lately, concerns of climate change have drawn the attention of researchers to study Arctic and Antarctica. Studies have shown that bacteria in Arctic and Antarctica have important roles for both ecosystem processes and global climate feedbacks (Melillo *et al*., 1995; Weintraub and Schimel, 2003; Wallenstein *et al*., 2007). For instance, the greater temperature increase in the Arctic compared to that in the Antarctica (IPCC, 1996) was found to be due to the large soil carbon pool and the carbon breakdown by predominant bacteria (Oechel and Vourlitis, 1994). Therefore, the Inter-governmental Panel on Climate Change (IPCC) has selected the Arctic and Antarctica as areas of special concern in their third assessment (IPCC, 2001).

Few studies on bacterial diversity in Arctic lake samples (Carlsson and Caron 2001; Graneli *et al*., 2004; Lindstrom *et al*., 2005), marine samples (Llobet Brossa *et al*., 1998; Sahm and Berninger, 1998; Ravenschlag *et al*., 1999; Ravenschlag *et al*., 2001; Bano *et al*., 2004), terrestrial samples (Zhou *et al*., 1997; Wartiainen *et al*., 2003; Kobabe *et al*., 2004; Nemergut *et al*., 2005; Neufeld and Mohn, 2005; Wallenstein *et al*., 2007) and glacier samples (Sharp *et al*., 1999; Skidmore *et al*., 2000; Wadham *et al*., 2004; Kastovska *et al*., 2005; Kastovska *et al*., 2007; Mindl *et al*., 2007) have been reported. These studies suggested that Arctic may contain substantial bacterial diversity. The bacterial diversity might varied between samples, as terrestrial samples were more diverse compared to other samples (Zhou *et al*., 1997). Furthermore, there might be similarity or differences in bacterial communities between samples. For instance, *δ-proteobacteria*, sulphate reducing bacteria, and *Bacteroidetes* were dominant in marine samples (Llobet Brossa *et al*., 1998; Sahm *et al*., 1998; Ravenschlag *et al*., 1999; Ravenschlag *et al*., 2001; Bano *et al*., 2004). On the other hand, methane-oxidizing bacteria, *Cyanobacteria*, *β-proteobacteria*, *δ-*

proteobacteria, *Acidobacteria* and *Fibrobacteria* were dominant in terrestrial samples (Zhou *et al*., 1997; Wartiainen *et al*., 2003; Kobabe *et al*., 2004; Nemergut *et al*., 2005; Neufeld and Mohn, 2005; Wallenstein *et al*., 2007). These bacteria played distinct and important roles in their habitats (Ravenschlag *et al*., 1999; Belnap and Lange, 2001; Kubeckova *et al*., 2002; Dubey *et al*., 2006).

Nonetheless, most of the bacteria in Arctic soils and sediments still remain unexplored due to the limitations in conventional culture-dependent methods (Hammond, 1995; Rappe and Giovannoni, 2003). Hence, it is necessary to know the composition of bacterial in the Arctic and also to get a better understanding of the correlation of these bacteria with their environmental variables: pH (Baath and Anderson, 2003; Lindstrom *et al*., 2005; Yannarell and Triplett, 2005; Fierer and Jackson, 2006) and salinity (Giovannoni and Rappe, 2000; Crump *et al*., 2004).

Ny-Ålesund, Norway (78 ºN, 11 ºE) is located in the Arctic Circle (Figure 1.1). The Dasan Station (78˚ 55' N, 11˚ 56' E) that is situated on the high Arctic island of Spitsbergen in Ny-Ålesund (Figure 1.2), includes tundra, alluvial plain and a plant protection area, and these areas are bounded by glaciers and sea. Dasan Station is inhabited by various animals such as barnacle geese, eider ducks, terns, kittiwakes, reindeers, foxes and the occasional visit of the polar bear (Korea Polar Research Institute). In general, the bacterial diversity in the Arctic soils and sediments might be influenced by the cold temperatures, plants detritus, human activities and the output of animals in the Arctic.

In this study, polymerase chain reaction-denaturing gradient gel electrophoresis (PCR-DGGE) was used to analyse the bacterial diversity in different types of Arctic samples (beach soil, terrestrial soils, inland lake bank sediments, marine sediments, melt lake sediment and periglacier soils). PCR-DGGE is a time saving and inexpensive culture-independent molecular approach (Nakatsu, 2007). The genomic DNA from the soils and

sediments were extracted using a DNA extraction kit for higher yield and better quality of DNA. Bacterial 16S rRNA gene fragments were amplified using a nested PCR and were separated by DGGE. The DGGE banding profiles were then statistically analyzed using Primer 6 multivariate data analysis package (Plymouth Marine Laboratory, UK), in order to determine the similarities within the bacterial community, and their correlation to the environmental variables (pH and salinity). Finally, 16S rRNA gene fragment analysis and phylogenetic analysis on well-defined DGGE bands were performed to identify the dominant species of bacteria in the samples.

1.1 Objectives of this study

- To use DGGE to compare the bacterial diversity in Arctic soil and sediment samples collected from eighteen sites in Ny-Ålesund, Norway.
- To identify the bacteria represented by well-defined DGGE bands.
- To correlate the bacterial communities with the soil pH and salinity.

Figure 1.1: The geographical location of the Ny-Alesund, Norway accessed from Choi *et al*. (2008).

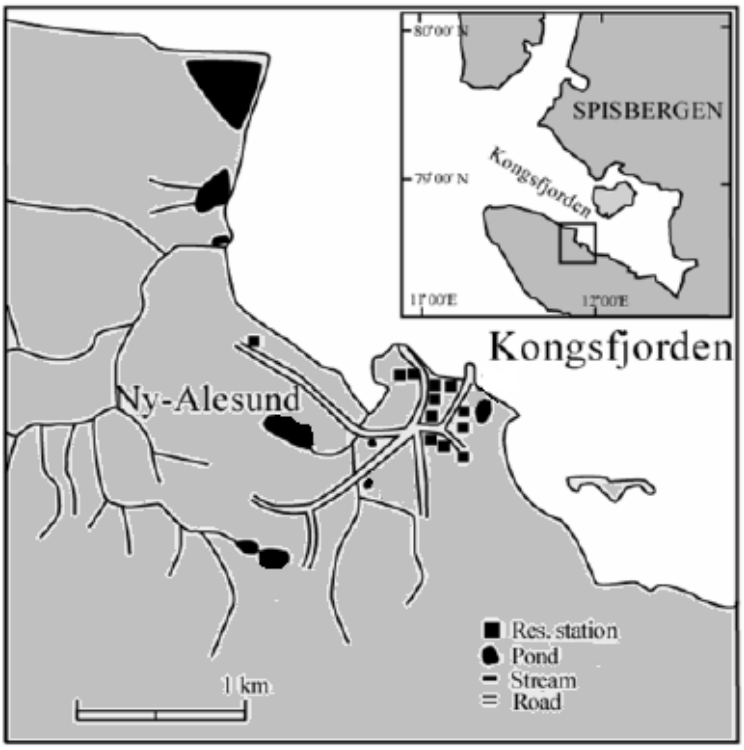

Figure 1.2: The location of Dasan Station, Ny-Alesund, Norway (Ki *et al*., 2006).