CHAPTER I

INTRODUCTION

Soil is a natural resource that, as a complex ecosystem, is home to a highly diverse range of prokaryotic and eukaryotic organisms, including plants, animals, and microorganisms. Bacteria, which are some of the smallest microorganisms, are one of the most abundant and diverse life forms in the soil ecosystem (Kennedy, 1999). Bacteria play important roles in biodegradation, and each bacterial species has its own particular roles and capabilities. Many bacteria are decomposers and other fix nitrogen into the ecosystem (Stark *et al.*, 2007). Thus, bacteria play an active and essential role in the control of nutrient cycles in the soil. Moreover, bacteria and other microorganisms, such as fungi and actinomycetes, participate in soil aggregation and toxin degradation. Bacteria can degrade different substances; therefore, their survival depends on the concentrations and distribution of various substances in their habitat (Torsvik and Øvreås, 2002). Furthermore, different physical properties of the soil such as type of soil, temperature, pH, water content, chemical composition and accumulated chemical substances, will lead to variation and abundance of bacteria (O'Donnell and Gorres, 1999 and Johnsen *et al.*, 2001).

Proper management of soil resources environment should be adopted in order to obtain the full benefits from the soil efficiently and sustainably. Different use and practice of land can significantly alter soil properties, resulting in difference in abundance and diversity of soil bacteria (Monokrousos *et al.*, 2006 and Zhang *et al.*, 2006). At present, there are two approaches used to study soil microbial diversity, culture-independent and culture-dependent techniques. Traditionally, culture-dependent techniques can be applied to study soil bacteria. However, since only 0.01% of soil bacteria can be readily cultured *in vitro* (Kirk *et al.*, 2004), limited information can be obtained using only culture-dependent techniques. Molecular, or culture-independent, techniques offer a powerful and essential tool to detect, identify, and quantify soil bacteria.

This research investigated the impacts of land management on soil bacterial diversity in Thongphaphum District, Kanchanaburi Province. Bacterial diversity in soils from an organic farm, a chemically-intensive farm, and nearby forest was compared using culture-dependent and molecular methods. In culture-dependent analysis of bacterial diversity, soil bacteria colonies were cultured in growth media and subjected to viable counts. Ecophysiological index (EPI) values were obtained for different study sites. Molecular analysis of bacterial diversity included soil DNA extraction, amplification with polymerase chain reaction (PCR), cloning, and subsequent DNA sequencing for species identification. Phylogenetic trees were then constructed to compare soil bacterial diversity of 3 different sites. Some soil physical factors from 3 sites were also analyzed. Comparison of soil bacterial diversity from the study sites would consequently show impacts of differing land management on bacterial flora.

The thesis is organized as follows: Chapter II gives an overall review of relevant literature. Chapter III details the general methodologies applied in this studying soil bacterial diversity, including study site description, soil sampling, and collection. Chapter IV presents analysis of soil properties. Chapter V offers the culture-dependent study of total bacterial counts and bacterial community structure. Chapter VI presents molecular diversity of soil bacteria and also discusses the impact of different land use and management patterns on soil bacterial diversity. Finally, chapter VII concludes the research.