

CHAPTER VII

CONCLUSIONS

1. Investigations of soil physical factors and nutrients among the chemically-intensive farm, the organic farm and the forest showed significant differences in soil moisture and pH, as well as soil nutrients, namely soil organic matter, organic carbon, total nitrogen, and available phosphorus contents.
 - Soil moisture content from three study sites in the dry season was the lowest value in the forest and the highest in the chemically-intensive farm. However, similar values were observed in the wet season.
 - Soil pH was more acidic in the chemically-intensive soil than in the organic farm and the forest soils, respectively.
 - Soil texture among three sites was classified as sandy loam.
 - Soil organic carbon, organic matter and total nitrogen, were highest in the forest site, but slightly different between the chemically-intensive farm and the organic farm.
 - Available phosphorus was highest in the chemically-intensive farm.
 - C/N ratio was not significantly different among sites and seasons.
2. The bacterial communities obtained from soils in 3 different sites were dominated by the *r*-strategist bacteria.
3. No significant difference was found in bacterial numbers in both between sites and seasons. The CFU counts were highest in the forest site, followed by the chemically-intensive farm and the organic farm, respectively. However, the

CFU values were positively correlated with soil pH and soil nutrients (organic matter, organic carbon and total nitrogen) in all sites.

4. Ecophysiological index (EPI) values were not significantly different between sites and seasons, with higher values in the bacterial community of the organic farm soil than those of the chemically-intensive farm soil and the forest soil.
5. The phylogeny of soil bacterial in different sites was highly diverse. From the results of bacterial diversity, different land management influenced the bacterial diversity, due to the fact that there were large numbers of unique phylotypes in each site.
6. The clones were distributed into many groups, viz. *Alpha*, *Beta*, and *Gamma* *proteobacteria*, *Actinobacteria*, *Firmicutes*, *Bacteriodes*, *Planctomycetes*, and unidentified group.
7. Most of the clones belonged to the unidentified uncultured bacteria (57.14%), while others were classified as *Alpha* (8.57%), *Beta* (2.86%), and *Gamma* (7.14%) *Proteobacteria*, *Firmicutes* (12.86%), *Actinobacteria* (8.57%), *Bacteriodes* (1.43%), and *Planctomycetes* (1.43%).
8. The results showed that *Thermoanaerobacter* sp. was found only in the forest. *Cellulosimicrobium* sp. was found only in the organic farm and *Streptomyces* sp. was found only in the chemically-intensive farm.

9. The results of bacterial diversity indicate that different land managements affect the bacterial diversity because of large numbers of unique phylotypes specific to each site.