

CHAPTER 6

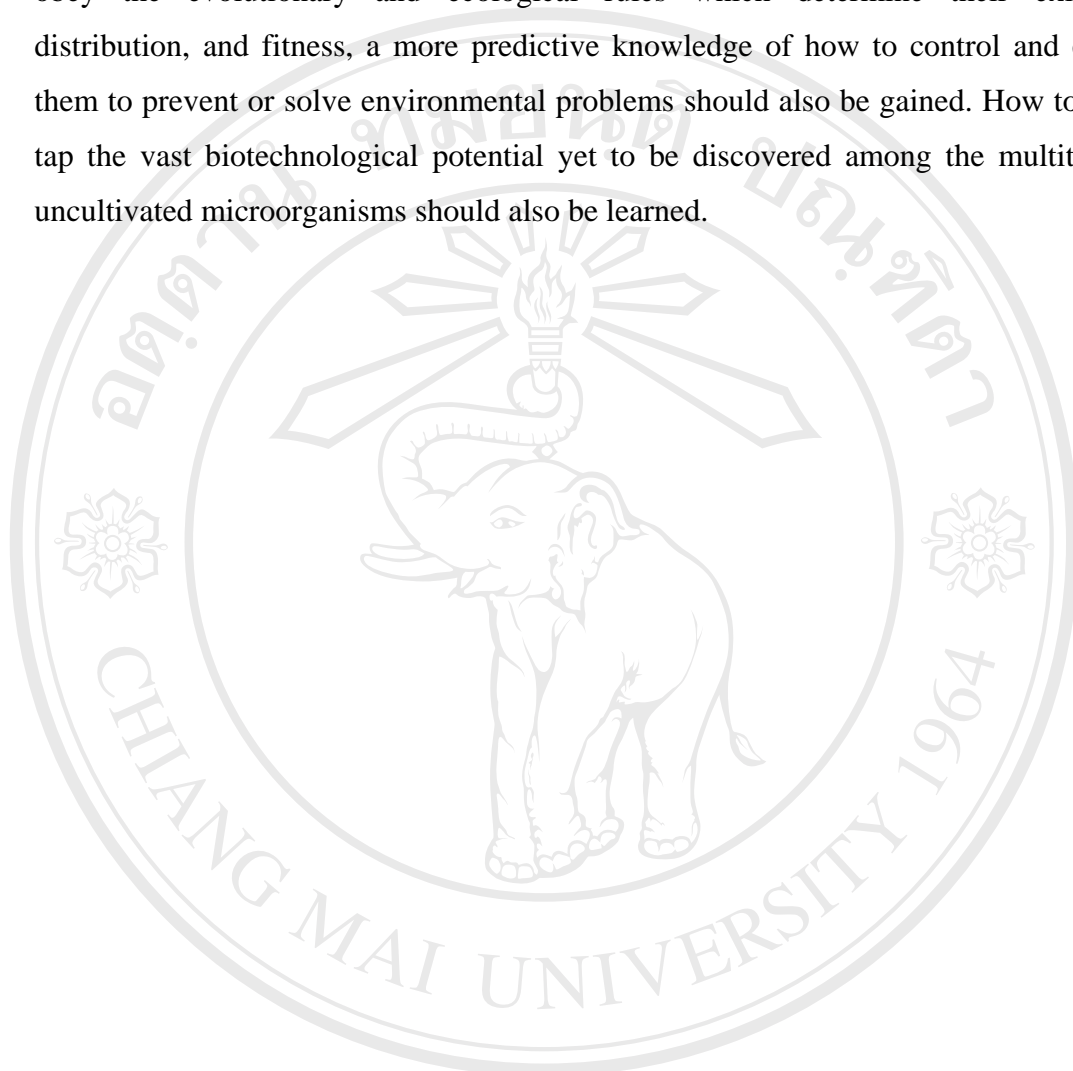
CONCLUSIONS AND RECOMMENDATIONS

The community diversity of thermophilic cyanobacterial mats from six geothermal springs was characterized. It was found that the 16S rDNA gene-defined diversity of all mats exceeded that observed by microscopy alone showing that the molecular data complemented established morphological methods, revealing an increased cyanobacterial diversity. From this increased molecular diversity, several morphologically similar yet molecularly distinct generic clusters were characterized which displayed both temperature and phylogeographic clines. It could be hypothesized that geographic barriers to dispersal may exist for some cyanobacterial species. As an untapped cyanobacterial resource, the hot springs in Thailand present a wide range of possibly unique species groups which could provide further insight into cyanobacterial evolution.

There is a clear trend to combine PCR-DGGE and other molecular techniques as well as microbiological and geochemical methods (Engelen *et al.*, 1998; Brinkhoff *et al.*, 1998; Radl *et al.*, 2005). This is important to reduce potential biases and limitations of the different techniques and hence to obtain a more realistic picture of microbial community structure and function.

However, molecular methods are attractive new tools in the kit of the microbial ecologist, especially when used in concert with more traditional methods. They permit detection of the specific microorganisms that are important in microbial communities, recognition of their evolutionary history, and determination of how they are organized to accomplish community function. By adopting the view of macroecologists and macroevolutionary biologists as they interpret their findings, microbial ecologists can see if unifying principles control the diversity, ecology, and evolution of all organisms, large and small. Prokaryotes define two of life's three primary evolutionary lineages; scientists know only a few of them, and yet their activities have a major influence on all ecosystems. Thus, a more predictive knowledge of the intricacies of natural microbial

communities upon which all life on Earth depends should be able to be gained. Since the microorganisms associated with applied problems (including disease) must also obey the evolutionary and ecological rules which determine their existence, distribution, and fitness, a more predictive knowledge of how to control and exploit them to prevent or solve environmental problems should also be gained. How to better tap the vast biotechnological potential yet to be discovered among the multitude of uncultivated microorganisms should also be learned.



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