

CHAPTER VI

CONCLUSIONS AND RECOMMENDATIONS

The results from this study provide preliminary information to help us understand the activities and diversity of bacteria populations in shrimp pond sediment during shrimp cultivation. Characteristics of sediment and bacterial communities in each shrimp pond were varied depending on locations and shrimp cultivation techniques. However, some of these characteristics were changed with a similar trend during shrimp cultivation. As shown in the result chapter, accumulation of organic matter during the cultivation crop had strongly related to ammonia and nitrite concentrations as well as the number of bacteria. The molecular technique, DGGE, illustrated that several types of bacteria were dominated in the sediment at the end of cultivation. Meanwhile, many dominant bacteria found in shrimp pond sediment were uncultured bacteria. The role of these bacteria is unclear hence further study is therefore needed.

Diversity of bacteria in shrimp pond within the same area, such as ponds R1 and R2 at Pathum Thani or ponds P1 and P2 at Ban Pho were similar in band pattern at the end of cultivation period. However, change in bacterial diversity as illustrated by an appearing or disappearing of DGGE bands were found especially when comparing DGGE bands of the first week with the following weeks.

Ozone treatment in an earthen shrimp pond at Ban Pho significantly reduced the number of bacteria in both water and sediment. However, the number of bacteria in ozone treated shrimp pond was increased to almost equal with the control (non-ozonated) after approximately 10 weeks of shrimp culture. It was found that ozone

affected the number of bacteria but not changed the diversity of bacterial population because the number of DGGE bands was similar in both ozone treatment and control ponds.

The most common bacteria in shrimp ponds were *Pseudomonas*, *Serratia*, *Vibrio*, *Marinobacter*, *Halomonas*, *Desulfovibrio* and *Bacillus*. However, diversity of bacteria in extensive shrimp ponds at Bang Khun Thian was much lower than that found in intensive shrimp ponds. Identification of bacteria by 16S rDNA database revealed that all dominant bacteria at Bang Khun Thian were marine bacteria. One of the dominant bacteria of Bang Khun Thian was *Vibrio harveyi* that is the well-known shrimp pathogenic bacteria.

An additional experiment involving nitrogen conversion in a chamber showed that, although nitrifying bacteria were not dominant in the sediment samples, activity of these bacteria could be detected under laboratory experiment. With this experiment, ammonia was released in a few hours after adding organic nitrogen source (as shrimp feed pellets). Nitrification process then converted ammonia to nitrite and nitrate. This was followed by denitrification in the sediment layer as indicated by ORP value according to nitrate reduction. From bacterial community data, we learnt that diverse groups of bacteria involved in this nitrogen cycling process. However, details study on each bacteria groups are needed for better understanding of shrimp pond ecosystem and consequently the improvement of shrimp pond management.

Recommendations

1. 16s rDNA PCR-DGGE is a very useful technique to illustrate the diversity of dominant bacteria in natural samples. However, additional techniques such as FISH (Fluorescence In Situ Hybridization) and real time PCR are needed if a specific minor group of bacteria is under interest. Classical techniques such as viable count using selective medium in specific condition *e.g.* aerobic and anaerobic are also useful in conjunction with molecular study.
2. Sediment characteristics could be varied even in the ponds of the same location. Further study might be expanded to shrimp farms with various salinity and pond management such as opened and closed systems.
3. The role of bacteria, especially dominant uncultured bacteria, in pond bottom ecosystem and biogeochemical cycle of shrimp pond is still unclear and therefore need to be investigated.