

Thesis Title	Dynamic of Microbial Community in Water Column of Pacific White Shrimp ( <i>Penaeus vannamei</i> ) Hatchery and Grow-Out Ponds
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### Abstract

In this work, there are three major parts that was investigated the correlation of microbial community and water quality during white shrimp (*Penaeus vannamei*) cultivation in hatchery and grow-out ponds by PCR-DGGE based on 16S rDNA gene; the first was focused on effect of *Spirulina* mats on water quality (*i.e.* total ammonia nitrogen, nitrite, and nitrate), water exchange rate and shrimp quality (*i.e.* survival rate, PL weight, PL length and survival rate in stress test) during shrimp cultivation in hatchery (during PL2-PL12 cultivation). From the result, it was found that in Set 2 (co-cultured shrimp with *Spirulina* mat) save 40% water exchange rate when compared to Set 1 (as control; only shrimp cultivation). Additionally, *Spirulina* mat also increased shrimp quality and growth when compared with control. This was an environmentally friendly process, due to the reduction in discharge into environment and the seawater used during the shrimp PL production process, which can certainly decrease the costs of shrimp production. The second was also focused on correlation between microbial community, water quality and shrimp quality, but in grow-out pond every month for 3 months. From the result, there were 22 OUTs (Operational Taxonomic Units) that would be divided in 3 groups of microorganism. The first dynamic consisted of the microbes that were found at all the time points investigated: *Nitrosomonas eutropha*, *Exiguobacterium SKRP 5*, and *Exiguobacteria* sp. CNJ771. The second group of microbial dynamics involved the replacement of *Flavobacteriales bacterium* with *Aquiflexum balticum*, both of which are bacteria involved in shrimp shell degradation.

In the first two months ( $W_0$  to  $W_2$ ), *Flavobacteriales bacterium* was responsible for the degradation of shrimp shells. However, as the salinity gradually decreased to 2 ppt (to control pathogens in the shrimp pond) and the temperature rose to 28.6 °C, the environmental conditions became optimal for *Aquiflexum balticum*; this finding might account for the observed replacement of *Flavobacteriales bacterium* with *Aquiflexum balticum*. The third group of microbial dynamics involved bacteria that were observed only at one time point, such as *Synechococcus* sp. Y0011 ( $W_0$ ), *Stenotrophomonas maltophilia* ( $W_3$ ), or at several time points, such as *Pseudomonas lanceolata* ( $W_0$  and  $W_3$ ) and *Burkholderia* sp. WBF2 ( $W_1$  and  $W_2$ ). As previously mentioned, although this third group of bacteria was not found at all of the time points investigated, they have an important role in balancing the shrimp culturing system, which is needed for a successful shrimp cultivation. The last was comparison of the microbial community between in hatchery and grow-out pond. From the result, it was found that *Vibrio* sp. was found only in hatcheries. However, that they were not found in grow-out ponds might be due to the effect of green water and low salinity in grow-out ponds. Moreover, nitrifying bacteria were found in both shrimp hatcheries and grow-out ponds. Some bacteria such as *Vibrio* sp., *Sphingomonas* sp. and *Pseudomonas* sp. were involved with shrimp health and nitrification in the system.

Key Words: DGGE/ Grow-out Pond/ Hatchery/ Microbial Community/ Shrimp/  
*Spirulina* Mat