Noppadol Kongkittayapun 2008: Variation in Adelphoparasite and Morphology of the Agarophyte, *Gracilaria salicornia* (C. Agardh) Dawson. Master of Science (Fisheries Science), Major Field: Fisheries Science, Department of Fishery Biology. Thesis Advisor: Associate Professor Anong Chirapart, Ph.D. 310 pages.

Changes in morphology of *Gracilaria salicornia* and its adelphoparasite were examined with reference to different habitats. The algal specimens were randomly collected during dry and monsoon seasons, from 11 sites of five provinces along the east and the west coast of the upper Gulf of Thailand. Some environmental parameters were also determined at each study sites. A general environment of the study sites appeared a distinct of an exposure, semi-exposed and sheltered conditions. The collections were done at Ko Si Chang, Ang-Sila, Sri Racha harbour, and Samaesan in Chonburi, Ban Phe in Rayong, Laem Sok, Laem Tien, and Ao Cho in Trat, Ta Mong Lai and Haad Wanakon in Prachuap Khiri Khan, and Haad Thung Wua Laen in Chumporn provinces. A part of the collected samples was preserved in 4% formaldehyde solution and another specimen was dried on herbarium sheets. Eight and seven morphological variables were used for analysis plants of *G. salicornia* and the adelphoparasite, respectively. The multivariate data set was analyzed by canonical discriminant analysis in combination with a clustering procedure. The multivariate data showed that morphology of *G. salicornia* is clustered into two groups: (1) specimens of Laem Sok, Laem Tien, Ta Mong Lai, Haad Thung Wua Laen, Ao Cho, Ang Sila, and Sri Racha harbor, (2) specimens of Ko Si Chang, Haad Wanakorn, Samaesan and Ban Phe. The adelphoparasite specimens could also divide into two groups: (1) Samaesan, Laem Sok and Ao Cho, and (2) Haad Thung Wua Laen, Ta Mong Lai and Haad Wanakorn. The discriminant analysis gave a very low degree of separation ($p = 0.05$).

This result was confirmed as detected by DNA-fragment polymorphism using RAPD technicque. Twenty primers were selected to amplify for DNA polymorphism. Twelve random primers, Meyer and Mitchell, OPA10, OPA11, OPK7, primer 2, primer 3, primer 5, primer 7, primer 9, primer 11, primer 14 and primer 15, successfully amplified the DNAs. The polymorphisms generated by these twelve primers were analyzed and then the cluster analysis was done using a program of TFPGA, and then tested by the UPGMA statistic program. The UPGMA test gave the similarity index values close to one for both *G. salicornia* and the adelphoparasite of all study sites. This result corresponded to the discriminant analysis obtained. This study showed that there have closely correlations among specimens of *G. salicornia* as well as the adelphoparasite grown at different habitats. On the other hand, theirs variation are thought to be mainly cause of changing in external environment of each study sites

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