Abstract

In 1960, the larvae of Anopheles minimus were found in the ditches, stream and rice field of entire Taiwan. The adult of this mosquito is anthrophagic , endophagic and endophilic. Therefore, it becomes the main vector for human malaria infection in

Taiwan. However, this mosquito was decreased after the island-wide spray of DDT for the malaria eradication campaign. Lin et al. reported that this mosquito

distributes only in 21 counties in southern and eastern Taiwan in 1997. Teng et al. (1998) analyzed the compositions in the water of the larval breeding sites located in such areas. They found that the NH4+ concentration is higher than that in Japan.

An.minimus in this island seems to adapt the higher concentration of NH4+ of water. They also showed that the B type of An.minimus is dominant form in these areas. Malaria infection is an important parasitic disease in Southeastern Asia. It may

cause problems in Taiwan due to thousands of the Taiwanese travelers to this areas each year. The surveillance of malaria vector is a necessary. In this study, attempt of collecting larvae and adults for Anopheles minimus we made at several locations in

Tainan, Pingtung, Hualian and Taitung. We found that this mosquito distributed only in Pingtung and Taitung with low density. This indicates that the changes of environment such as water pollution, plant fauna decreases around the stream and

This indicates that the changes of environment such as water pollution, plant fauna decreases around the stream and abundant rain brought by big storm may create suboptimal breeding conditions for An. minimus. The mosquitoes collected from Pingtung were identified to be A type of An. minimus based on the morphological characters of adults and larvae skin. The DNA fragment containing Internal transcribed spacer-ITS-2 and the flanking region was amplified, cloning and sequenced for An. minimus collected from Tainan and Pingtung. These mosquitoes were identified as A type of An. minimus because the similarity of nucleotide sequence is of 99-100% to that of A type. This result does not agree the report of Teng et al. (1998)

as mentioned previously. Because the sequence of same region is not available for type B, we need some B type specimen to be used for DNA extraction and the

gene amplification. This experiment will clarify the resolution power of ITS-2 and its flanking in the respect of distinguishing type A and B. The banding derived from rapid amplified polymorphisms DNA -PCR (RAPD-PCR) also showed that the An. minimus in three areas had similar genetic characters.

Key Word：Anopheles minimus、Form identification、Morphology、ITS-2、RAPD-PCR、Isozyme