GENETIC POLYMORPHISM IN DENGUE MOSQUITO *Aedes aegypti* (DIPTERA : Culicidae) BASED ON RAPD-PCR ANALYSIS

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INTRODUCTION

Dengue Hemorrhagic Fever (DHF) is major public health problem in Indonesia. Dengue fever is most important viral disease transmited to human by mosquito *Aedes aegypti* . *Aedes aegypti* is the principal vector for dengue virus, this vector is able to maintain the four serotypes of dengue viruses (DEN 1,2,3 and 4) in urban transmission cycle. More than 80.837 cases were reported through calendar year 2005 in Indonesia. One of the factors determining the high number of occurrences is the density vector (*Aedes aegypti*). The research on the genetic strain variability of *Aedes aegypti* must get a serious attention, since there is a correlation between the genetic strain variability and the adaptation for survival (Wallis *et al* (1984). Organism with higher variability will survive and regenerate more easely than those with lower variability. Vector insects with higher change of survival will have higher population. The more densely populated the vector, the higher its chance to run into humans. This is what cases the increasing number of occurrence of DHF cases and the expanding width of the infected area.

Based on above illustrations, therefore, a research on the genetic phenomena dealing with genetic variability (genetic polymorphism) of the dengue mosquito (*Aedes aegypti*). The genetic polymorphism level can be revealed by conducting an analysis on the DNA polymorphism with RAPD (Random Ampliified Polymorphic DNA). Since the discovery in 1990 of the RAPD technique, it has been extensively use for several purpose for example, individual or strain identification, genetic variation of population and the phylogenetic relationship (Thanananta *et al*, 1997). RAPD technique detects randomly amplified polymorphic DNA fragments in PCR with single arbitrary primer of 8-10 bp (Williams *et al*, 1990). The number of fragments amplified and the degree of polymorphism in eukaryotic species depend on the nucleotide sequence, the secondary structure and the number of primers used for each RAPD assay. These features of the

Based on table 1, the analysis of all DNA bands based on all location in the district of Jember, indicates that polymorphism level of *Aedes aegypti* DNA from Sumbersari is the highest level compared to the others sample location. The result of RAPD qualitative analysis showed that the polymorphism level of *Aedes aegypti* from Sumbersari, Patrang and Kaliwates were 73.7%, 72.2% and 64.3% respectively. The *Aedes aegypti* which have high polymorphism level are indicated high genetic variability. Having high genetic variability, the *Aedes aegypti* will have high survive and cause more population. The higher level of genetic diversity of an organism, the greater the range of tolerance to the organism in adapting to their habitats. The organism will have a high survival capacity compared to organisms with low levels of diversity. Insect vectors that have a high survival rate will have a total population of more than one generation to another. There is a relationship between the number of populations with high rates of infection. The sizes of DNA fragments of *Aedes aegypti* that are amplificated with five oligonucleotida (OPE 16, OPE 17, OPE 19, OPF 2 and OPF 4) were ranged from 163 bp-2622 bp and OPE 17 primer is more varied in amplify DNA. It indicates that complement genomic DNA region with primer OPE 17 more numerous and varied.

CONCLUSION

DNA samples of *Aedes aegpyti* which was amplified by using primer OPE 16, OPE 17, OPE 19, OPF 2 and OPF 4 range in size from 108 bp-2313 bp . OPE 17 primers to amplify genomic DNA of mosquitoes *Aedes aegpyti* is more varied. The polymorphism level of *Aedes aegypti* from Sumbersari, Patrang and Kaliwates showed a relatively high percentage (73.7%, 72.2% and 64.3%)

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