

DETECTION AND MOLECULAR ANALYSIS OF
MEGALOCYTVIRUS IN OYSTERS
(*CRASSOSTREA IREDALE*) IN MALAYSIA.

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State of Sabah and Johor, Malaysia which are located in the middle of one the twelve mega biodiversity sites in the world were among the most important locations for aquaculture industries especially the cultivation of oysters (*Crassostrea iredalei*). However, in 2012, mass mortalities of oysters and mussels affecting few farms in Marudu Bay, Sabah were observed. Since the location of the cultivation area for both mussels and oysters are in the same area and the suspected virus, *Megalocytivirus* can be transmitted via water therefore, it is presumed that the problem could also affect the cultivation and yield of oysters. The aim of this study was to investigate the presence/absence of *Megalocytivirus* in oysters (*Crassostrea iredalei*) from Marudu Bay, Sabah and Masai, Johor using molecular approach. In this study, a total of 80 oyster's samples were tested for the presence of *Megalocytivirus*. The DNA were amplified by Single-step and nested PCR amplification using primer that amplified MCP gene of *Megalocytivirus* selectively and generally. The PCR analysis showed that the occurrence of

Megalocyttivirus in Sabah and Johor were 27.5% and 0% respectively. Sequencing and phylogenetic analysis of the representative samples from Sabah suggested that strains of the virus belong to the *Megalocyttivirus* genus in the *Iridoviridae* family. Thus, this study demonstrated the first detection of *Megalocyttivirus* in a new organism, oyster (*Crassostrea iredalei*).