

ABSTRACT

Fazira Putri Utami. 24020221140086. "Isolation and Molecular Characterization of PUFA-Producing Thraustochytrids from Karimunjawa Mangrove Forest Litter Samples using 18S rRNA Gene". Under the guidance of Dr. rer. nat. Anto Budiharjo, S. Si., M. Biotech and Dr. Drs. Wijanarka, M.Si.

PUFA (*Polyunsaturated fatty acids*), especially DHA, are essential for the food, health, animal feed, aquaculture, and pharmaceutical industries as essential components for brain development, the nervous system, and immunity. Global demand for PUFA sources continues to increase, while availability from traditional sources such as fish oil is increasingly limited. This occurs due to marine environmental pollution that causes a decrease in the quality and quantity of fish oil, so alternatives such as Thraustochytrids from the tropical marine environment of Karimunjawa waters. Thraustochytrids are a group of heterotrophic protists that have been known to produce significant amounts of PUFA, especially *docosahexaenoic acid* (DHA). This study aims to obtain Thraustochytrid isolates originating from the Karimunjawa mangrove environment obtained using two isolation methods, namely *pollen baiting* and *direct plating*, while also providing taxonomic information and phylogenetic relationships through 18S rRNA gene sequencing analysis. Data analysis was carried out by collecting data and comparing it with the results of studies that have been carried out based on existing references. Based on the research results, 8 isolates were found with 5 isolates originating from the *direct method* and 3 isolates from the *pollen baiting* method. The results of screening using Sudan Black B showed that isolate SK14.1, SK6.2, SK9C, and SK12 had a high lipid content. The isolation of Thraustochytrids from Karimunjawa was identified as *Aurantiochytrium*, based on the macroscopic and microscopic morphological characteristics that had been carried out. Isolates SK10.2 and SK14.1 were identified as one of the *Aurantiochytrium* sp. groups, with the highest sequence similarity to *Aurantiochytrium* sp. 76%.

Keywords: Thraustochytrids, PUFA, Direct method, Pollen baiting, *Aurantiochytrium* sp.