

## ABSTRACT

Thraustochytrids, a group of heterotrophic protists, predominantly found in mangrove ecosystems associated with organic material. Thraustochytrids represents as a valuable source for biotechnological applications since Thraustochytrids are highly valued for their remarkable polyunsaturated fatty acid (PUFA) production like DHA, carotenoid, squalene, and hydrolytic enzymes such as amylase, protease, and cellulase. This study aimed to explore and identify the genetic diversity of Thraustochytrids from mangrove leaves and sediment within Setiu Wetland, Malaysia. Isolates were obtained using baiting method, and characterized through morphological and molecular analysis using Thraustochytrid-specific primers. Three isolates from decayed mangrove leaves and one from sediments were obtained. Morphologically, the isolates exhibited white to orange color, jelly-like to creamy texture, and cellular structures were sub-globose, aggregated, and granular under microscopic observation. Molecular analyses revealed that one isolate L332 from *Rhizosphora* mangrove leaves belongs to *Ulkenia* sp., two isolates, L412 and L531 from *Aegiceras* mangrove leaves affiliated to *Schizochytrium* sp., one isolate S421 from sediment showed close phylogenetic relationships to *Botryochytrium* sp., while one isolate L532 from *Aegiceras* mangrove leaves remains unclassified within *Thraustochytriaceae* but closely related to *Schizochytrium* sp. This finding highlights the underexplored diversity of Thraustochytrids in mangrove ecosystems, also their morphological variabilities, which support molecular identification and reveals potential novel lineages.

*Keywords:* Thraustochytrids, Mangrove, Setiu Wetland, *Ulkenia* sp., *Schizochytrium* sp., *Botryochytrium* sp.