

Abstract of thesis presented to the Senate of Universiti Malaysia Terengganu in  
fulfilment of the requirement of Master of Science

**MOLECULAR AND MORPHOLOGICAL ANALYSES OF  
THE TWO-SPINED YELLOW-TAIL STARGAZER, *Uranoscopus cognatus*  
(CANTOR, 1849) FROM EAST COAST OF PENINSULAR MALAYSIA  
AND WEST COAST OF THAILAND**

**NUR ILHAM SYAHADAH BINTI MOHD YUSOFF**

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**Main Supervisor : Tan Min Pau, Ph. D**  
**Co Supervisor : Tun Nurul Aimi binti Mat Jaafar, Ph. D**  
**Faculty : Faculty of Fisheries and Food Science**

The Benthic species, though ecologically important, are vulnerable to genetic and population size reduction due to impacts from fishing trawls. This study was the first to assess the population of the two-spined yellow-tail stargazer (*Uranoscopus cognatus*) within the Indo-West Pacific (IWP) for unveiling its genetic pool and population structure. Samples were collected from the west coast of Thailand (WCT) and east coast of peninsular Malaysia (ECPM), where 231, 171 and four individuals were sequenced at the partial mitochondrial DNA cytochrome c oxidase subunit 1 gene (COI), the single-copy nuclear DNA recombination activating gene 1 (RAG1) and whole mitogenome sequences, respectively. Results demonstrated that the population of *U. cognatus* was moderate to highly diversified (haplotype diversity,  $H = 0.490$  to  $0.900$ , nucleotide diversity,  $\pi = 0.0010 - 0.0034$ ) except for sampling station (ST) 1 and 14. The low diversity level, however, was apparent only in the matrilineal COI marker ( $H = 0.118 - 0.216$ ;  $\pi = 0.0004 - 0.0008$ ), possibly due to stochastic factors or anthropogenic stressors. A common source of origin or ancestor of *U. cognatus* within IWP was apparent; however, prolonged vicariance by the Indo-Pacific Barrier has partitioned them into the separate stock unit. Genetic propinquity of *U. cognatus* from the ECPM with those from the central and west Java, Indonesia was evident, suggesting a long-range dispersal ability of its planktonic larvae by 2,500 km apart, which was mediated by the seasonally reversing monsoon currents. Mitochondrial

DNA uncovered a recent population expansion while nuclear DNA uncovered an older population expansion. The final partitioned nucleotide alignment of the whole mitogenome comprises 14,098 base pairs (bp) and is the third representative for its genus that consists of 55 formally described species to date. Phenotypic divergence of the allopatric *U. cognatus* was also observed, characterised by the heterogeneous interorbital fossa length, upper jaw length, postorbital length and the number of supracleithral spines, with the former two indicating evolution in the premaxillary protrusion that is possibly associated with the mechanism for upper jaw movement in biomechanical feeding approaches. This present study suggests that *U. cognatus* population within the IWP is still healthy and abundant (except ST1 and 14) and that the two stock units identified will undergo a specific resource management program.

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**ANALISA MOLEKULAR DAN MORFOLOGI DARI IKAN DEPU-LAUT  
SPINA, *Uranoscopus cognatus* (CANTOR, 1849) DARI PANTAI TIMUR  
SEMENANJUNG MALAYSIA DAN PANTAI BARAT THAILAND**

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**Penyelia Utama : Tan Min Pau, Ph. D**  
**Penyelia Bersama : Tun Nurul Aimi binti Mat Jaafar, Ph. D**  
**Fakulti : Fakulti Perikanan dan Sains Makanan**

Spesies bentik, walaupun penting dari segi ekologi, terdedah kepada pengurangan saiz genetik dan populasi akibat kesan daripada pukut tunda nelayan. Kajian ini adalah yang pertama untuk menilai populasi ikan depu-laut (*Uranoscopus cognatus*) dalam Pasifik Indo-Barat (IWP) bertujuan mengungkap kumpulan genetik dan struktur populasinya. Sampel dikumpulkan dari pantai barat Thailand (WCT) dan pantai timur semenanjung Malaysia (ECPM), di mana 231, 171 dan empat individu masing-masing diujukkan pada DNA mitokondria sitokrom c oksidase subunit 1 gen (COI), satu salinan DNA nuklear gen pengaktifan penggabungan semula 1 (RAG1) dan keseluruhan urutan mitogenom. Hasil kajian menunjukkan bahawa populasi *U. cognatus* adalah sederhana hingga tinggi dalam kepelbagaian genetiknya (kepelbagaian haplotaip,  $H = 0.490$  hingga  $0.900$ , kepelbagaian nukleotida,  $\pi = 0.0010 - 0.0034$ ) kecuali stesen persempelan (ST) 1 dan 14. Walau bagaimanapun, tahap kepelbagaian genetik yang rendah hanya kelihatan pada penanda matrilineal COI ( $H = 0.118 - 0.216$ ;  $\pi = 0.0004 - 0.0008$ ), mungkin disebabkan faktor stokastik atau tekanan antropogenik. Satu sumber asal atau nenek moyang *U. cognatus* dalam IWP dapat dilihat; bagaimanapun, penjarakan berpanjangan yang dihalang Indo-Pasifik memisahkan mereka menjadi unit stok yang berasingan. Persamaan genetik *U. cognatus* dari ECPM dengan yang berasal dari Jawa tengah dan barat, Indonesia terbukti menunjukkan kemampuan penyebaran jarak jauh larva planktoniknya sejauh

2.500 km dan dimediasi pembalikan arus monsun secara berulang kali. DNA mitokondria menemukan pengembangan populasi baru, sementara DNA nuklear menemukan pengembangan populasi terdahulu. Sekatan akhir penjajaran nukleotida keseluruhan mitogenom terdiri daripada 14,098 pasangan asas (bp) dan merupakan wakil ketiga daripada 55 spesies untuk genusnya yang diperihalkan secara rasmi sehingga kini. Perbezaan fenotipik oleh alopatrik *U. cognatus* juga diperhatikan, yang dicirikan oleh perbezaan panjang fossa interorbital, panjang rahang atas, panjang postorbital dan bilangan tulang supracleithral, dengan dua yang pertama menunjukkan evolusi dalam tonjol premaksilari, kemungkinan berkaitan dengan mekanisma pergerakan rahang atas berhubung dengan pendekatan biomekanik untuk makan. Kajian ini menunjukkan bahawa populasi *U. cognatus* dalam IWP masih sihat dan banyak (kecuali ST1 dan 14), dan dua unit stok dikenal pasti akan menjalani program pengurusan sumber daya tertentu.