

**GENETIC DIVERSITY, POPULATION STRUCTURE AND DEMOGRAPHIC
PATTERNS OF *Nemipterus furcosus* IN THE EASTERN COAST OF
PENINSULAR MALAYSIA**

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School : School of Fisheries and Aquaculture Sciences

Nemipterus furcosus is a non-migratory and commercially important demersal fish in the Southeast Asia region, including the eastern coast of Peninsular Malaysia. The total catch of this species has increased significantly due to increased trawling activities. Although several aspects such as parasitic infections, taxonomy and species identification have been well studied, information on the genetic structure and evolutionary process of this species are presently unknown. Here we investigated the population structure and demographic history of six populations of *N. furcosus* in the eastern coast of Peninsular Malaysia using mitochondrial cytochrome oxidase subunit I (COI) and nuclear Rhodopsin (RHO) markers. A total of 654 base pair (bp) of COI gene and 528 base pair (bp) of RHO gene were sequenced. High mean haplotypes diversity ($h = 0.83989$ for COI, $h = 0.90414$ for RHO) and low mean nucleotide diversity ($\pi =$

0.00521 for COI, $\pi = 0.24090$ for RHO) were observed in all *N. furcosus* populations, suggesting occurrence of population expansion. Our results also revealed significant negative values for both neutrality tests and mismatch distribution analysis, which further supported the recent expansion event. Despite lower F_{ST} value was observed between neighboring populations such as BR-PK ($F_{ST} = 0.04724$, $p < 0.05$ for COI, $F_{ST} = 0.00693$, $p < 0.05$ for RHO) and KMM-KTN populations ($F_{ST} = 0.05564$, $p < 0.05$ for COI, $F_{ST} = 0.09657$, $p < 0.05$ for RHO), our AMOVA and Isolation By Distance analyses showed substantial genetic variation among all populations between regions. These results were further supported by Bayesian STRUCTURE analysis and Maximum Likelihood (ML) phylogenetic tree, which have revealed three major clusters in six *N. furcosus* populations. We hypothesized that increased in fishing activities; modification of geographical structure of ocean bed during Pleistocene era may have contributed to the population expansion process. We also speculated that the larval dispersion through strong oceanic current during monsoon season and the geographical distance between populations might have shaped the current genetic structure of *N. furcosus* populations. Ultimately, to obtain a better insight on the genetic variability of *N. furcosus*, multidisciplinary research covering a wider distribution range such as population genetics, life history, physiological adaption and ecological behavior of this species are necessary.

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**KEPELBAGAIAN GENETIK, STRUKTUR POPULASI DAN CORAK
DEMOGRAFI *Nemipterus furcosus* DI PANTAI TIMUR SEMENANJUNG
MALAYSIA**

MOHAMAD HAFIZ FARHAN BIN ABDUL RASID

Jun 2016

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Pusat Pengajian : Pusat Pengajian Sains Perikanan dan Akuakultur

Nemipterus furcosus merupakan ikan demersal yang tidak berhijrah dan mempunyai nilai komersialnya di rantau Asia terutamanya di pantai timur Semenanjung Malaysia. Jumlah tangkapan ikan ini telah meningkat disebabkan oleh peningkatan aktiviti bot pukat tunda. Walaupun banyak kajian seperti jangkitan parasit, taksonomi, dan pengenalan identiti spesis telah dijalankan ke atas spesis ikan ini, namun tiada kajian yang dijalankan berkenaan struktur genetik dan proses evolusi terhadapnya. Oleh itu, kami telah menyasat struktur populasi dan sejarah demografi bagi enam populasi *N. furcosus* di pantai timur Semenanjung Malaysia dengan menggunakan penanda molekul mitokondria cytochrome oxidase subunit I (COI) dan nuklear rhodopsin (RHO). Sebanyak 654 jujukan DNA bagi gen COI dan 528 jujukan DNA bagi gen RHO telah berjaya diujukkan. Purata kepelbagaian haplotaip yang tinggi ($h = 0.83989$ untuk COI,

$h = 0.90414$ untuk RHO) dan purata kepelbagaian nukleotida yang rendah ($\pi = 0.00521$ untuk COI, $\pi = 0.24090$ untuk RHO) telah diperhatikan dalam populasi *N. furcosus* dimana ianya mencadangkan berlakunya pengembangan populasi. Keputusan kajian kami juga mendedahkan nilai-nilai negatif yang signifikan bagi kedua-dua ujian neutraliti dan analisis taburan tidak sepadan, yang turut menyokong proses perkembangan populasi ini. Walaupun nilai F_{ST} yang lebih rendah diperhatikan antara populasi berdekatan seperti BR-PK ($F_{ST} = 0,04724$, $p < 0.05$ untuk COI , $F_{ST} = 0,00693$, $p < 0.05$ untuk RHO) dan populasi KMM-KTN ($F_{ST} = 0,05564$, $p < 0.05$ untuk COI , $F_{ST} = 0,09657$, $p < 0.05$ untuk RHO) , namun analisis AMOVA dan pengasingan berdasarkan jarak telah menunjukkan variasi genetik yang besar di kalangan semua populasi yang dibandingkan diantara rantau-rantau. Keputusan ini turut disokong oleh analisis STRUKTUR Bayesian dan pokok filogenetik Kemungkinan Maksimum (ML), yang telah mendedahkan tiga kelompok utama dalam enam populasi *N. furcosus*. Kami beranggapan bahawa peningkatan dalam aktiviti menangkap ikan; pengubahsuaian struktur geografi dasar laut semasa era Pleistocene mungkin menyumbang kepada proses perkembangan populasi. Kami juga membuat spekulasi bahawa penyebaran larva melalui lautan yang berarus deras pada musim tengkujuh dan jarak geografi antara populasi telah membentuk struktur genetik semasa populasi *N. furcosus* . Akhirnya , untuk mendapatkan gambaran yang lebih baik mengenai kepelbagaian genetik *N. furcosus* , penyelidikan pelbagai disiplin meliputi pelbagai taburan yang lebih luas seperti genetik populasi, sejarah hidup , adaptasi fisiologi dan tingkah laku ekologi spesies ini adalah diperlukan.