

## KERAGAMAN GENETIK IKAN GLODOK, *Periophthalmus kalolo* (Lesson, 1831), DARI HUTAN MANGROVE CILACAP, CILACAP, JAWA TENGAH BERDASARKAN GEN MITOKONDRIA 16S rRNA

Andhika Dwi Novitasari  
21/474471/BI/10712

Dosen Pembimbing: Prof. Dra. Tuty Arisuryanti, M.Sc., Ph.D.

### INTISARI

Indonesia memiliki hutan mangrove terbesar di dunia dan ikan glodok adalah organisme yang seringkali dijumpai di ekosistem tersebut, salah satunya yaitu spesies *Periophthalmus kalolo* (Lesson, 1831). Penelitian tentang keragaman genetik ikan glodok menggunakan gen mitokondria 16S rRNA di Hutan Mangrove Cilacap, Cilacap, Jawa Tengah belum pernah dilakukan. Oleh karena itu, pada penelitian ini akan dilakukan analisis keragaman genetik ikan glodok dari Hutan Mangrove Cilacap, Cilacap, Jawa Tengah menggunakan gen mitokondria 16S rRNA. Penelitian ini menggunakan metode PCR dengan menggunakan primer 16Sar dan 16Sbr melalui tahapan isolasi DNA, amplifikasi DNA, elektroforesis, purifikasi, dan sekuensing. Hasil penelitian ini dianalisis menggunakan GeneStudio, BLAST, MESQUITE, MEGA, DnaSP, BEAST, NETWORK, dan GenAIEx. Hasil penelitian menunjukkan bahwa dari 5 sampel ikan glodok yang diteliti menunjukkan adanya keragaman genetik, yaitu terdapat 5 haplotipe dan dari panjang fragmen 598 bp terdapat 10 situs polimorfik yang terdiri dari 5 *parsimony informative sites* dan 5 *singleton sites*, serta nilai keragaman haplotipe sebesar  $1,000 \pm 0,01600$ , nilai keragaman nukleotida sebesar  $0,00836 \pm 0,00198$ , dan jarak genetik berkisar 0,17%-1,35%. Hasil analisis interpopulasi (data yang diteliti dengan data pembandingan dari *GenBank*) juga menunjukkan adanya keragaman genetik, yaitu dari 9 sampel yang dianalisis terdapat 6 haplotipe dan dari panjang fragmen 598 bp terdapat 10 situs polimorfik yang terdiri dari 7 *parsimony informative sites* dan 3 *singleton sites*, serta nilai keragaman haplotipe sebesar  $0,8889 \pm 0,091$ , nilai keragaman nukleotida sebesar  $0,00641 \pm 0,00118$ , dan jarak genetik berkisar 0,00%-1,35%. Analisis filogenetik menghasilkan 3 *clade* dengan jarak genetik berkisar 0,42%-1,18%. Kelima sampel ikan glodok yang diteliti berada pada *clade A* (MCL-12), *clade B* (MCL-15), dan *clade C* (MCL-2, MCL-11, dan MCL-14). Hasil analisis jejaring haplotipe dan analisis dengan *Principal Coordinate Analysis* (PCoA) mendukung data pohon filogenetik dan jarak genetik yang menunjukkan *clade A* dan *clade B* memiliki jarak lebih dekat daripada *clade C*. Hasil penelitian ini diharapkan dapat digunakan untuk menyusun pustaka gen mitokondria 16S ikan glodok yang dapat digunakan sebagai landasan konservasi ikan glodok di Indonesia.

**Kata kunci:** gen mitokondria 16S, keragaman genetik, mangrove, *Periophthalmus kalolo*

**GENETIC VARIATION OF COMMON MUDSKIPPER, *Periophthalmus kalolo* (Lesson, 1831), FROM CILACAP MANGROVE FOREST, CILACAP, CENTRAL JAVA BASED ON MITOCHONDRIAL 16S rRNA GENE**

Andhika Dwi Novitasari  
21/474471/BI/10712

Supervisor: Prof. Dra. Tuty Arisuryanti, M.Sc., Ph.D.

**ABSTRACT**

Indonesia has the largest mangrove forest in the world, where mudskippers are among the organisms commonly found in this ecosystem, including the common mudskipper, *Periophthalmus kalolo* (Lesson, 1831). Research on the genetic variation of common mudskippers using the mitochondrial 16S rRNA gene in the Cilacap Mangrove Forest, Cilacap, Central Java, had not been conducted. Therefore, this research aimed to analyze the genetic variation of common mudskippers from the Cilacap Mangrove Forest, Cilacap, Central Java, using the mitochondrial 16S rRNA gene. This research used the PCR method with 16Sar and 16Sbr primers through the stages of DNA isolation, DNA amplification, electrophoresis, purification, and sequencing. The results of this study were analyzed using GeneStudio, BLAST, MESQUITE, MEGA, DnaSP, BEAST, NETWORK, and GenAIEx. Based on the research results, intrapopulation analysis revealed genetic variation. For five samples with 598 bp fragment length, five haplotypes were revealed with ten polymorphic sites (five parsimony informative sites and five singleton sites). Haplotype diversity of *P. kalolo* was  $1.000 \pm 0.01600$  whereas nucleotide diversity was  $0.00836 \pm 0.00198$ . In addition, the genetic distance varied from 0.17%-1.35%. The results of the interpopulation also revealed genetic variation. For nine samples (five from this study and four from GenBank) with 598 bp fragment length, six haplotypes were revealed with ten polymorphic sites (seven parsimony informative sites and three singleton sites). Haplotype diversity of *P. kalolo* was  $0.8889 \pm 0.091$  whereas nucleotide diversity was  $0.00641 \pm 0.00118$ . In addition, the genetic distance varied from 0.00%-1.35%. Phylogenetic analysis generated 3 clades with genetic distance ranging from 0.42%-1.18%. Sample MCL-12 was in clade A, sample MCL-15 was in clade B, and three samples (MCL-2, MCL-11, and MCL-14) were in clade C. The results of haplotype network analysis and Principal Coordinate Analysis (PCoA) supported the phylogenetic tree data and genetic distance, which showed that clade A and clade B are closer than clade C. The results from this study are expected to assembly mitochondrial 16S gene library which is important to be implemented in conservation.

**Keywords:** genetic variation, mangrove, mitochondrial 16S gene, *Periophthalmus kalolo*