

**KERAGAMAN GENETIK KATAK BARAM, *Pulchrana baramica*
(Boettger, 1990), POPULASI JAWA, SUMATERA DAN KALIMANTAN
BERDASARKAN GEN MITOKONDRIA 16S**

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INTISARI

Indonesia merupakan negara tropis yang memiliki keanekaragaman hayati yang tinggi termasuk keanekaragaman jenis amfibi. Pada kelompok amfibi sering dijumpai *cryptic species* yang dapat menimbulkan kerancuan proses identifikasi. Salah satu jenis amfibi yang ditemukan di Indonesia yaitu *Rana baramica* dengan nama spesies terbaru *Pulchrana baramica*. Spesies ini memiliki daerah distribusi yang luas termasuk Pulau Jawa. Spesies *P. baramica* merupakan satu-satunya spesies dari Genus *Pulchrana* yang ditemukan di Pulau Jawa. Sejak tahun 1998 hingga saat ini belum ada penelitian yang membahas mengenai data molekuler Populasi Pulau Jawa dari spesies ini. Dengan daerah distribusi yang luas serta memiliki populasi yang terpisah oleh lautan maka penelitian molekuler ini digunakan untuk mengidentifikasi kedudukan taksonomi spesies *P. baramica* dari populasi Kalimantan, Sumatera, dan Jawa serta untuk melihat variasi genetik interpopulasi dari sampel yang diteliti berdasarkan gen mitokondria 16S dan menyediakan data molekuler spesies *P. baramica* populasi Pulau Jawa yang sebelumnya belum ada. Pada penelitian ini digunakan metode PCR dengan primer L2606 dan H3056. Data yang diperoleh dianalisis menggunakan *software* DNASTAR, BLAST, Mesquite, MegaX, DnaSP, Network dan BEAST. Analisis data sekuens dilakukan untuk mendapatkan data nilai similaritas, variasi genetik, jarak genetik dan rekonstruksi pohon filogeni. Hasil penelitian menunjukkan seluruh sampel katak yang diteliti teridentifikasi ke dalam familia Ranidae. Dua diantara 10 sampel teridentifikasi merupakan spesies *P. baramica* (Herp 0009 dan Herp 0012), sedangkan 8 sampel teridentifikasi *multiple species* dengan jarak genetik 3,50-5,45%. Data tersebut didukung dengan tingginya jumlah haplotipe dan *variable sites* yaitu jumlah haplotipe 8 dan 34 *variable sites* (31 *parsimony informative sites* dan 3 *singleton sites*) yang terdiri dari 29 transisi dan 5 transversi serta nilai *haplotype diversity* $0,956 \pm 0,059$ dan nilai *nucleotide diversity* $0,0384 \pm 0,0056$. Hasil dari penelitian ini diharapkan dapat memberikan informasi genetik yang dapat digunakan pada penelitian selanjutnya dan memberikan kontribusi untuk menyusun pustaka gen mitokondria 16S rRNA (*16S mitochondrial DNA library*) *Pulchrana baramica* di Indonesia, khususnya Pulau Jawa.

Kata Kunci: *Pulchrana baramica*, keanekaragaman genetik, 16S rRNA

GENETIC DIVERSITY OF THE BARAM RIVER FROG, *Pulchrana baramica* (Boettger, 1990), POPULATIONS IN JAVA, SUMATRA AND KALIMANTAN BASED ON 16S MITOCHONDRIAL GENE

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ABSTRACT

Indonesia is a tropical country with a high level of biodiversity, including a diverse range of amphibian species. Within the amphibian group, cryptic species are often encountered, leading to confusion in the identification process. One of the amphibian species found in Indonesia is *Pulchrana baramica* formerly known as *Rana baramica*. This species has a wide distribution range, including Java Island. *P. baramica* is the only species of the *Pulchrana* genus found on Java Island. Since 1998 until now, no research has been conducted on the molecular data of the Java Island population of this species. Given its wide distribution area and the fact that its populations are separated by the ocean, molecular research is being conducted to identify the taxonomic position of *P. baramica* from populations in Kalimantan, Sumatra, and Java, as well as to examine the interpopulation genetic variations based on the mitochondrial gene 16S, and provide molecular data for the population of *P. baramica* on Java Island that was previously lacking. PCR method with L2606 and H3056 primers was used in this study. The obtained data were analyzed using DNASTAR, BLAST, Mesquite, MegaX, DnaSP, Network, and BEAST software. Sequence data analysis was performed to obtain data on similarity values, genetic variations, genetic distances, and phylogenetic tree reconstruction. The research results indicated that all the examined frog samples were identified within the Ranidae family. Two out of the 10 samples were identified as *P. baramica* species (Herp 0009 and Herp 0012), while the remaining eight samples were identified as multiple species with a genetic distance of 3.50-5.45%. These findings were supported by the high number of haplotypes and variable sites, with a total of 8 haplotypes and 34 variable sites (31 parsimony informative sites and 3 singleton sites), consisting of 29 transitions and 5 transversions. The haplotype diversity value was calculated as 0.956 ± 0.059 , and the nucleotide diversity value was 0.0384 ± 0.0056 . The results of this study are expected to provide genetic information that can be utilized in further research and contribute to the construction of a 16S mitochondrial DNA library for *Pulchrana baramica* in Indonesia, particularly on Java Island.

Key words: *Pulchrana baramica*, genetic diversity, 16S rRNA