

Studi filogenetik *Microhyla heymonsi* vogt, 1911 anura: Microhylidae dari Pulau Sumatra berdasarkan analisis gen 16s rRNA mitokondria = Phylogenetic study of Sumatran *Microhyla heymonsi* vogt 1911 anura Microhylidae based on 16s rRNA mitochondrial gene analysis

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Abstrak

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*Microhyla heymonsi* merupakan spesies yang memiliki distribusi sangat luas, mulai dari Taiwan, China, India, Indochina, Semenanjung Malaysia, hingga Sumatra. Spesies dengan distribusi sangat luas seringkali mengandung spesies kriptik akibat pemisahan geografis sehingga terjadi isolasi reproduksi, mutasi gen, dan evolusi. Penelitian ini bertujuan untuk mengetahui hubungan filogenetik antara spesies *M. heymonsi* dari Sumatra dan luar Sumatra, serta nilai jarak genetik antara kedua kelompok spesies tersebut. Nilai jarak genetik yang digunakan sebagai batas pembeda spesies adalah 3. Sekuens DNA didapatkan melalui proses DNA Barcoding dan kemudian dilakukan studi filogenetik melalui analisis Unweighted Pair Group Method with Arithmetic Mean, Neighbourhood Joining, Maximum Likelihood, dan Bayesian Inference. Hasil menunjukkan bahwa spesies *M. heymonsi* dari Sumatra membentuk satu clade besar tersendiri pada pohon filogeni dari semua metode analisis dengan didukung nilai bootstrap yang signifikan. Nilai jarak genetik antara *M. heymonsi* Sumatra dengan *M. heymonsi* Singapura dan Malaysia masih di bawah 3. Nilai jarak genetik antara *M. heymonsi* Sumatra dengan *M. heymonsi* Thailand, Myanmar, Vietnam, dan China telah melebihi angka 3.

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Abstract *Microhyla heymonsi* is a species that has very wide distribution, ranging from Taiwan, China, India, Indochina, Peninsular Malaysia, to Sumatra. Species with a very wide distribution often contain cryptic species due to the geographical barrier resulting in reproductive isolation, gene mutation, and evolution. This study aims to determine the phylogenetic relationship between *M. heymonsi* species from Sumatra and outside Sumatra, as well as the value of genetic distance between the two groups of species. The genetic distance threshold as a species delimitation is 3. DNA sequences were obtained through the process of DNA barcoding and then phylogenetic studies were performed through analysis of Unweighted Pair Group Method with Arithmetic Mean, Neighborhood Joining, Maximum Likelihood, and Bayesian Inference. The results show that the *M. heymonsi* species from Sumatra form a large single clade on the phylogenetic tree of all analytical methods with significant bootstrap values. The genetic distance value of *M. heymonsi* Sumatra with *M. heymonsi* Singapore and Malaysia is still below 3. The genetic distance values between *M. heymonsi* Sumatra and *M. heymonsi* Thailand, Myanmar, Vietnam and China have exceeded 3.