

## **Filogenetik dan Estimasi Waktu Divergensi *Heliconia* spp. di Yogyakarta Berdasarkan Sekuen Gen *matK***

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### **INTISARI**

*Heliconia* spp. atau pisang hias merupakan salah satu komoditas florikultur yang banyak dibudidayakan di Indonesia. Pemanfaatan *Heliconia* spp. sebagai tanaman hias perlu diimbangi dengan upaya konservasi dan pemuliaan plasma nutfah. Studi filogenetik perlu dilakukan untuk mengatasi keterbatasan studi keragaman fenotip dan genotip. Gen *maturaseK* (*matK*) telah banyak digunakan dalam mengidentifikasi spesies, merekonstruksi pohon filogenetik dan mengestimasi waktu divergensi pada tanaman. Penelitian ini bertujuan untuk mengetahui hubungan kekerabatan dan estimasi waktu divergensi *Heliconia* spp. di Kota Yogyakarta. Penelitian ini menggunakan metode PCR dengan primer *matK*-1RKIM-f dan *matK*-3FKIM-r. Data sekuen DNA dianalisis menggunakan GeneStudio, BLAST, Mesquite, MEGA 11, DnaSP, NETWORK dan BEAST. Analisis data sekuen DNA gen *matK* dilakukan untuk mendapatkan data similaritas, jarak genetik, pohon filogenetik dan kronogram estimasi waktu divergensi. Hasil penelitian menunjukkan 17 sampel *Heliconia* spp. teridentifikasi ke dalam dua spesies, yaitu *H. acuminata* (10 sampel) dan *H. meridensis* (7 sampel) dengan jarak genetik 0,0000-0,0062. Hasil penelitian juga menunjukkan terdapat variasi genetik antar spesies. Hubungan kekerabatan *Heliconia* spp. Kota Yogyakarta tergolong kelompok monofiletik dan waktu divergensi diperkirakan terjadi pada zaman *Late Cretaceous* 72 Mya (~74-69 Mya).

**Kata kunci:** *Heliconia*, *matK*, monofiletik, *bootstrap*, waktu divergensi

**Phylogenetic and Divergence Time Estimation of *Heliconia* spp.  
from Yogyakarta Inferred by *matK* Gene**

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**ABSTRACT**

*Heliconia* spp. or ‘pisang hias’ is one of the most widely cultivated floricultural commodities in Indonesia. Utilization of *Heliconia* spp. as an ornamental plant needs to be balanced with conservation and breeding of germplasm. Phylogenetic studies need to be carried out to overcome the limitations of phenotypic and genotypic diversity studies. The *maturaseK* (*matK*) gene has been widely used in identifying species, constructing phylogenetic trees and estimating divergence times in plants. This study aims to determine the phylogenetics and estimate time divergence of *Heliconia* spp. in Yogyakarta City. This research using PCR method with *matK*-1RKIM-f and *matK*-3FKIM-r primers. Sequences data was analyzed using GeneStudio, BLAST, Mesquite, MEGA 11, DnaSP, NETWORK and BEAST. The analysis was conducted to obtained similarity, genetic distance, phylogenetic trees, and chronogram of estimated divergence. The results revealed that 17 samples of *Heliconia* spp. were identified in two species, namely *H. acuminata* (10 samples) and *H. meridensis* (7 samples) with genetic distance 0,0000-0,0062. The results also demonstrated the appearance of genetic variation between species. The relationship between *Heliconia* spp. in Yogyakarta city was classified as a monophyletic group, and the divergence time was estimated to have occurred in *Late Cretaceous* 72 Mya (~74-69 Mya).

**Keywords:** *Heliconia*, *matK*, monophyletic, *bootstrap*, divergence time