ANALISIS FILOGENETIK LAMIACEAE BERDASARKAN BARKODE *ITS, matK,* DAN *rbcL* SECARA *IN SILICO*

SKRIPSI

Diajukan sebagai salah satu syarat untuk memperoleh
gelar Sarjana Sains pada Program Studi Biologi

Oleh:
Chayra Endlessa
NIM. 2004280

PROGRAM STUDI BIOLOGI
FAKULTAS PENDIDIKAN MATEMATIKA DAN ILMU PENGETAHUAN ALAM
UNIVERSITAS PENDIDIKAN INDONESIA
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2024

LEMBAR HAK CIPTA

ANALISIS FILOGENETIK LAMIACEAE BERDASARKAN BARKODE *ITS, matK,* DAN *rbcL* SECARA *IN SILICO*

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Skripsi yang diajukan untuk memenuhi salah satu syarat memperoleh gelar Sarjana Sains pada Program Studi Biologi Fakultas Pendidikan Matematika dan Ilmu Pengetahuan Alam

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LEMBAR PENGESAHAN

CHAYRA ENDLESSA

ANALISIS FILOGENETIK LAMIACEAE BERDASARKAN BARKODE *ITS, matK,* DAN *rbcL* SECARA *IN SILICO*

Disetujui dan disahkan oleh

Pembimbing I,

Prof. Topik Hidayat, M.Si., Ph.D.

NIP. 197004101997021001

Pembimbing II,

Dr. Hj. Siti Sriyati, M.Si.

NIP. 196409281989012001

Mengetahui,

Ketua Program Studi Biologi

Dr. Wahyu Surakusumah, M.T.

NIP. 197212301999031001

LEMBAR PERNYATAAN

Dengan ini saya menyatakan bahwa skripsi dengan judul "Analisis Filogenetik Lamiaceae Berdasarkan Barkode *ITS, matK,* dan *rbcL* secara *In Silico*" ini beserta seluruh isinya adalah benar-benar karya saya sendiri. Saya tidak melakukan penjiplakan atau pengutipan dengan cara-cara yang tidak sesuai dengan etika ilmu yang berlaku dalam masyarakat keilmuan. Atas pernyataan ini, saya siap menanggung risiko/sanksi apabila di kemudian hari ditemukan adanya pelanggaran etika keilmuan atau ada klaim dari pihak lain terhadap keaslian karya saya ini.

Bandung, Juni 2024

Yang membuat pernyataan,

Chayra Endlessa

NIM. 2004280

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Dalam proses penulisan skripsi ini, penulis menyadari bahwa masih terdapat ruang untuk perbaikan. Oleh karena itu, saran dan kritik yang membangun sangat diharapkan agar skripsi ini dapat menjadi referensi yang lebih baik di masa mendatang. Semoga hasil dari skripsi ini dapat memberikan kontribusi positif dalam pengembangan ilmu pengetahuan bagi penulis dan pembaca yang berkepentingan.

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Chayra Endlessa

NIM. 2004280

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Penulis,

Chayra Endlessa

NIM. 2004280

ANALISIS FILOGENETIK LAMIACEAE BERDASARKAN BARKODE *ITS, matK,* DAN *rbcL* SECARA *IN SILICO*

ABSTRAK

Lamiaceae kerap dimanfaatkan dalam pengobatan tradisional dan modern tetapi rentan terhadap adulterasi dan eksploitasi. Pendekatan filogenetik mampu menjadi solusi alternatif untuk mencegah adulterasi dan menjaga biodiversitas Lamiaceae. Namun, rekonstruksi filogenetik Lamiaceae terhambat karena kemiripan morfologi, diskrepansi filogenetik berbasis morfologi dan DNA, serta kurangnya studi filogenetik genus tertentu. Studi ini bertujuan untuk mendapatkan informasi filogenetik Lamiaceae berdasarkan barkode DNA inti (*ITS*) dan kloroplas (*matK* dan *rbcL*) parsial untuk mencegah adulterasi dan mendukung konservasi Lamiaceae. Daftar genus dicari di *Barcode of Life Data System.* Sekuens DNA parsial 52 spesies perwakilan 11 genus, dan *Spathodea campanulata* sebagai *outgroup,* didapat dari *GenBank* NCBI. Pensejajaran dan pemotongan DNA dilakukan sebelum empat pohon filogenetik *maximum parsimony* direkonstruksi (tiga berbasis satu barkode dan satu gabungan ketiganya) dengan MEGA 11. Analisis pohon meliputi prinsip *parsimony, bootstrapping,* indeks konsistensi (CI), dan indeks retensi (RI). Rerata sekuens terpanjang diperoleh *matK* (785.6 pb), tingkat homologi tertinggi *rbcL* (83.5%), dan jumlah situs *parsimony-informative* terbanyak *ITS* (40.3%). Setiap pohon mempunyai CI rendah (~0.5) dan RI tinggi (>0.5). Setiap barkode secara terpisah menunjukkan pola pengelompokan yang serupa pada genus yang berkerabat dekat tetapi memisahkan beberapa spesies dari genusnya. Gabungan ketiga barkode mengoreksi posisi spesies yang terpisah dan mengelompokkan Lamiaceae ke dalam enam klad monofiletik (*bootstrap* >70%): *Callicarpa*; *Scutellaria*; *Clerodendrum, Lamium,* dan *Stachys*; *Salvia*; *Thymus, Origanum,* dan *Mentha*; *Orthosiphon* dan *Ocimum*. Pohon filogenetik gabungan mampu mencegah adulterasi dan mendukung konservasi Lamiaceae karena memberikan informasi mengenai kekerabatan spesies target adulterasi yang bermanfaat untuk mengidentifikasi spesies adulteran dan menemukan spesies alternatif dengan sifat minyak esensial yang serupa.

Kata kunci: adulterasi, barkode DNA, filogenetik, Lamiaceae.

IN SILICO PHYLOGENETIC ANALYSIS OF LAMIACEAE BASED ON ITS, matK, AND rbcL DNA BARCODES

ABSTRACT

Lamiaceae, often utilized in traditional and modern medicine, are vulnerable to adulteration and exploitation. A phylogenetic approach can prevent these issues and conserve Lamiaceae biodiversity. However, reconstructing the phylogeny of Lamiaceae is hindered by morphological similarities, discrepancies between morphological and DNA data, and limited phylogenetic studies on certain genera. This study aimed to obtain phylogenetic information of Lamiaceae based on partial nuclear (ITS) and chloroplast (matK and rbcL) DNA barcodes to prevent adulteration and promote the conservation of Lamiaceae. Genera were obtained from the Barcode of Life Data System. Partial DNA sequences from the NCBI GenBank for 52 species across 11 genera (with Spathodea campanulata as the outgroup) were used. Sequences were aligned and trimmed to reconstruct four maximum parsimony trees using MEGA 11 (three based on one barcode and one combined). Tree analysis included parsimony principle, bootstrapping, consistency index (CI), and retention index (RI). The longest average sequence was found in matK (785.6 bp), highest homology in rbcL (83.5%), and most parsimony-informative sites in ITS (40.3%). Trees had low CI (~0.5) and high RI (>0.5). While individual barcodes showed similar genus groupings, they separated some species from their genera. Combining the barcodes corrected these positions, grouping Lamiaceae into six monophyletic clades (bootstrap >70%): Callicarpa; Scutellaria; Clerodendrum, Lamium, and Stachys; Salvia; Thymus, Origanum, and Mentha; Orthosiphon and Ocimum. The combined tree aids in preventing adulteration and conserving Lamiaceae by providing phylogenetic information on adulterated species, which is useful in identifying adulterants and finding alternative species with similar essential oil properties.

Keywords: *adulteration, DNA barcodes, phylogenetics*, Lamiaceae.

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