

**ANALISIS VARIASI GENETIK *Etlingera loerzingii* ENDEMIK SUMATERA
DENGAN MENGGUNAKAN PENANDA ISSR**

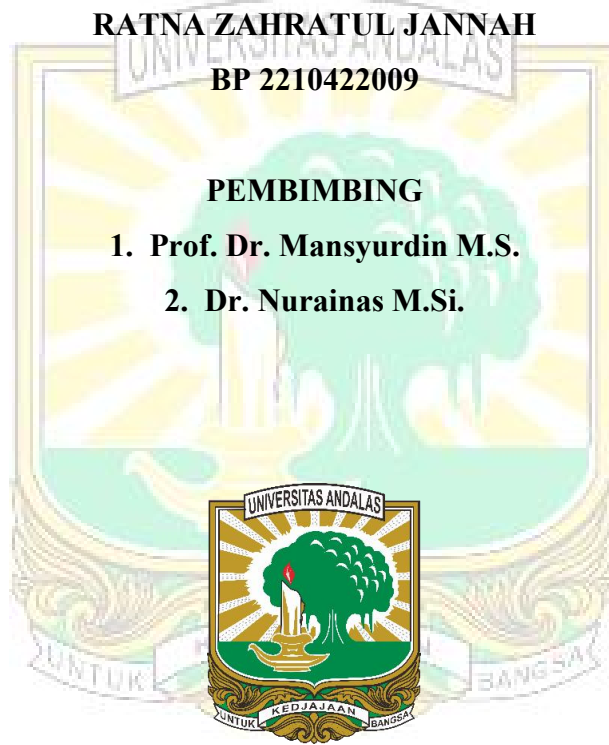
SKRIPSI SARJANA BIOLOGI

OLEH:

**RATNA ZAH RATUL JANNAH
BP 2210422009**

PEMBIMBING

- 1. Prof. Dr. Mansyurdin M.S.**
- 2. Dr. Nurainas M.Si.**



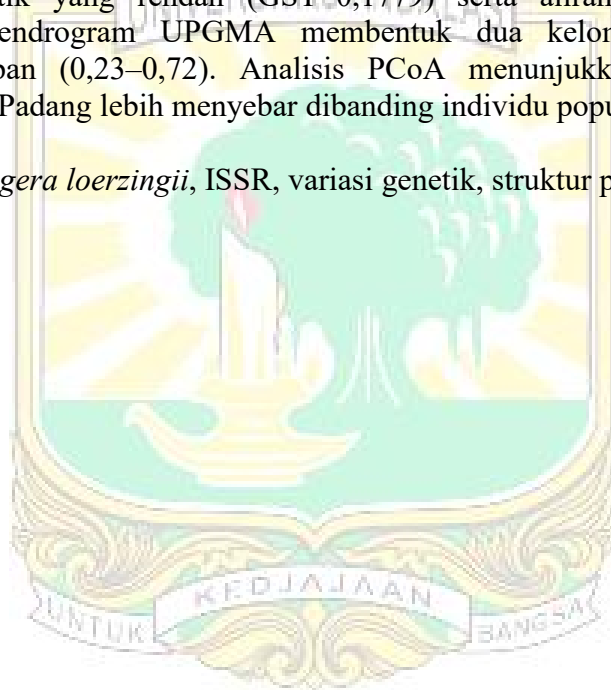
**DEPARTEMEN BIOLOGI
FAKULTAS MATEMATIKA DAN ILMU PENGETAHUAN ALAM
UNIVERSITAS ANDALAS, PADANG**

2026

ABSTRAK

Etlingera loerzingii (Zingiberaceae) merupakan tumbuhan endemik Sumatera dan berstatus rentan sehingga kajian variasi genetik menggunakan penanda *Inter-Simple Sequence Repeat* (ISSR) diperlukan sebagai dasar penyusunan strategi konservasi. Penelitian ini bertujuan menganalisis variasi genetik intrapopulasi dan interpopulasi serta struktur populasi *E. loerzingii* di Sumatera Barat pada dua lokasi Padang dan Sijunjung, masing-masing sebanyak 10 individu. Dari 15 primer ISSR yang diuji didapatkan tiga primer dengan polimorfisme tertinggi ($\geq 80\%$) (ISSR1, ISSR5, dan HB8) menghasilkan 44 lokus pada 20 individu. Nilai variasi genetik intrapopulasi tergolong rendah Padang ($H=0,2427$) dan Sijunjung ($H=0,2070$) dengan populasi Padang lebih tinggi di banding populasi Sijunjung. Nilai intrapopulasi lebih tinggi dari interpopulasi dengan ($H_s=0,2249$) lebih tinggi dari ($DST=0,0487$) dan nilai diferensiasi genetik yang rendah ($GST=0,1779$) serta aliran gen yang tinggi ($N_m=2,3113$). Dendrogram UPGMA membentuk dua kelompok utama pada koefisien kemiripan (0,23–0,72). Analisis PCoA menunjukkan pola distribusi individu populasi Padang lebih menyebar dibanding individu populasi Sijunjung.

Kata kunci: *Etlingera loerzingii*, ISSR, variasi genetik, struktur populasi, konservasi



ABSTRACT

Etlingera loerzingii (Zingiberaceae) is an endemic plant species of Sumatra classified as Vulnerable. Therefore, an assessment of its genetic variation using Inter-Simple Sequence Repeat (ISSR) markers is necessary to provide a scientific basis for developing appropriate conservation strategies. This study aimed to analyze intrapopulation and interpopulation genetic variation and the population structure of *E. loerzingii* in West Sumatra. Samples were collected from two populations, Padang and Sijunjung, with 10 individuals obtained from each population. Of the 15 ISSR primers initially screened, three primers exhibiting the highest levels of polymorphism ($\geq 80\%$), namely ISSR1, ISSR5, and HB8, were selected and generated 44 loci across 20 individuals. Intrapopulation genetic variation was relatively low in both populations, with genetic diversity values of $H = 0.2427$ in Padang and $H = 0.2070$ in Sijunjung. The Padang population exhibited a higher level of genetic variation than the Sijunjung population. Genetic variation within populations was greater than that among populations, as indicated by the higher within-population genetic diversity ($H_s = 0.2249$) compared with the among-population genetic diversity ($D_{ST} = 0.0487$). The populations also showed a low level of genetic differentiation ($G_{ST} = 0.1779$) and a high level of gene flow ($N_m = 2.3113$). The UPGMA dendrogram grouped the individuals into two major clusters at similarity coefficients ranging from 0.23 to 0.72. Principal Coordinate Analysis (PCoA) showed that individuals from the Padang population were more widely dispersed than those from the Sijunjung population.

Keywords: *Etlingera loerzingii*, ISSR, genetic variation, population structure, conservation

