

# BUKTI KORESPONDENSI ARTIKEL JURNAL

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## Genetic Diversity and Relationship of Durian (*Durio spp.*) Germplasm Based on the Internal Transcribed Spacer (ITS) Region: *In Silico* Analysis

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### ABSTRACT


Durian (*Durio spp.*) is a germplasm with a relatively high species diversity, with an estimated 27 species worldwide. However, the existence of several species has been threatened. This study aimed to reconstruct the DNA barcode of the durian and its relatives (*Durio spp.*) and analyze the genetic diversity and its relationship based on the internal transcribed spacer (ITS) region. Sixteen sequences of durians ITS were collected from GenBank (NCBI) and analyzed *in silico* using the BLAST, MultiAlin, and MEGA-X software, then reconstructed phylogenetically by the UPGMA and Maximum Likelihood methods. The results show that the ITS region of *Durio spp.* has a base length of about 702 bp, where several mutations occur, substitution (transversion and transition) and indel (insertion and deletion). At the nucleotide level, this germplasm shows a relatively high diversity of 0.065. The cluster analyses (UPGMA and Maximum Likelihood) can separate this germplasm into four clusters and five main clades, respectively. In this study, *D. zibethinus*, the most popular species in the *Durio* genus, is closely related to *D. lowianus* and far from *D. griffithii*. This information is beneficial as reference data to support durian conservation and breeding programs, locally and globally, especially in Indonesia.

**Keywords:** Chloroplast DNA, Breeding, Durian, Genetic diversity, Phylogenetic

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