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Molecular diversity of exotic durian (*Durio* spp.) germplasm: a case study of Kalimantan, Indonesia

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Abstract

Background: Durian of Indonesia, specifically *Durio zibethinus*, is a potential agricultural commodity for domestic and international markets. However, its quality is still less competitive or significantly lower to fulfill the export market, compared to a similar one from other countries. This study aimed to determine and analyze the genetic diversity and relationship of the exotic durian (*Durio* spp.) germplasm originally from Kalimantan, Indonesia, using the *rbc*L marker.

Results: Based on this marker, the durian germplasm has a low genetic diversity (π %=0.24). It may strongly correspond with the variability sites or mutation present in the region. In this case, the *rbcL* region of the durian germplasm has generated 23 variable sites with a transition/transversion (Ti/Tv) bias value of 1.00. However, following the phylogenetic and principal component analyses, this germplasm is separated into four main clades and six groups, respectively. In this case, *D. zibethinus* was very closely related to *D. exleyanus*. Meanwhile, *D. lowianus* and *D. excelsus were* the farthest. In further analysis, 29 durians were very closely related, and the farthest was shown by *Durian Burung* (*D. acutifolius*) and *Kalih Haliyang* (*D. kutejensis*) as well as *Pampaken Burung Kecil* (*D. kutejensis*) and *Durian Burung* (*D. acutifolius*) with a divergence coefficient of 0.011. The Pearson correlation analysis confirms that 20 pairs of individual durians have a strong relation, shown by, e.g., *Maharawin Hamak* and *Durian Burung* as well as *Mantuala Batu Hayam* and *Durian Burung Besar*.

Conclusion: While the durian has a low genetic diversity, the phylogenetic analyses revealed that this germplasm originally from Kalimantan, Indonesia, shows unique relationships. These findings may provide a beneficial task in supporting the durian genetic conservation and breeding practices in the future, locally and globally.

Keywords: DNA barcoding, Genetic diversity, Malvaceae, Phylogenetic relationship, Plant breeding

