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Research Article

Phylogenetic relationship of superior durian (*Durio zibethinus*) cultivars native to South Kalimantan, Indonesia¹

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ABSTRACT

Durian, especially *Durio zibethinus*, is an agricultural commodity with high economic value, both in local and global markets. This study aimed to determine the genetic diversity, relationships and correlation of superior cultivars of *D. zibethinus* ('Likol', 'Sahang' and 'Si Japang') native to South Kalimantan, Indonesia, using the *rbcL* marker, and compare them with other 48 cultivars from the GenBank database. All durian *rbcL* markers were analyzed using the MEGA-X software and phylogenetically reconstructed using two approaches: maximum likelihood (ML) and neighbor-joining (NJ). The durian phylogenetic tree was assessed by bootstrap analysis, and their relationships by Pearson's correlation and principal component analysis. The durian showed a low genetic diversity ($\pi\% = 0.056$); however, unique relationships were revealed. Following the *rbcL* region, this germplasm was grouped into five clades using ML and NJ. In this case, 'Si Japang' and 'Sahang' showed to be closely related to 'T16' from Malaysia, whereas 'Likol' was related to 'Monthon' from Thailand. However, based on the genetic divergence analysis, 'Sahang' had the farthest relationship with three durians from Thailand ('Metnai Kanyao', 'Chok Loi' and 'Malet Ar-Ri').

RESUMO

Relação filogenética de cultivares superiores de durian (*Durio zibethinus*) nativas de Kalimantan do Sul, Indonésia

O durian, especialmente *Durio zibethinus*, é uma commodity agrícola com alto valor econômico, tanto no mercado local quanto global. Objetivou-se determinar a diversidade genética, relações e correlação de cultivares superiores de *D. zibethinus* ('Likol', 'Sahang' e 'Si Japang') nativas de Kalimantan do Sul, Indonésia, usando o marcador *rbcL*, e compará-las com outras 48 cultivares do banco de dados GenBank. Todos os marcadores durian *rbcL* foram analisados usando o software MEGA-X e filogeneticamente reconstruídos utilizando-se duas abordagens: máxima verossimilhança (ML) e agrupamentos vizinhos (NJ). A árvore filogenética do durian foi avaliada por análise de bootstrap, e suas relações pela correlação de Pearson e análise de componentes principais. O durian apresentou baixa diversidade genética ($\pi\% = 0.056$); no entanto, relações únicas foram reveladas. Segundo a região *rbcL*, esse germoplasma foi agrupado em cinco clados, utilizando-se ML e NJ. Nesse caso, 'Si Japang' e 'Sahang' mostraram-se intimamente relacionadas com 'T16' da Malásia, enquanto 'Likol' relacionou-se com 'Monthon' da Tailândia. No entanto, com base na análise de divergência genética, 'Sahang' apresentou o relacionamento mais distante com três durians da Tailândia ('Metnai Kanyao', 'Chok Loi' e 'Malet Ar-Ri').

KEYWORDS: Breeding program, Borneo Island, genetic

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