The Molecular Diversity-based ISSR of Durio tanjungpurensis Originating from West Kalimantan, Indonesia

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Abstrak

Diversitas Molekuler Berbasis ISSR pada Durio tanjungpurensis Asal Kalimantan Barat, Indonesia. Durian Tengkurak (Durio tanjungpurensis Navia) adalah salah satu spesies langka yang eksotis dari suku Malvaceae. Durian tersebut bernilai penting untuk konservasi plasma nutfah dan berpotensi sebagai sumber daya genetik untuk pengembangan durian di masa depan. Tujuan penelitian adalah mengetahui keragaman molekuler D. tanjungpurensis asal Kalimantan Barat berdasarkan penanda Inter Simple Sequence Repeat (ISSR). Sepuluh primer ISSR digunakan untuk mengetahui keragaman genetik 60 individu Durian Tengkurak dari enam populasi endemik alami D. tanjungpurensis. Parameter keragaman genetik didasarkan pada data biner pita DNA produk PCR, yaitu ada atau tidak- ada pita. Hasil penelitian menunjukkan bahwa rata-rata jumlah alel, rata-rata jumlah efektif alel, diversitas genetik, indeks informasi Shannon, jumlah polimorfik lokus, dan persentase polimorfik lokus berturut-turut adalah 1,53, 1,29, 0,17, 0,26, 77,83 dan 52,59. Analisis ragam molekuler (AMOVA) menunjukkan keragaman genetik yang lebih tinggi di dalam populasi (65%) dibandingkan antar populasi (35%). Analisis gugus menggunakan metode UPGMA berdasarkan matriks keserupaan Dice dan analisis koordinat utama digunakan untuk mengelompokkan semua individu populasi ke dalam tiga kelompok, yaitu grup 1 (Hutan Rejunak dan Tembaga), grup 2 (Bukit Merindang), dan grup 3 (Hutan Rawak, Bukit Sagu 1 dan Bukit Sagu 2). Analisis lebih lanjut terhadap struktur populasi menggunakan program STRUCTURE menyatukan grup 2 dan 3 ke dalam satu grup utama. Penelitian ini berhasil mengungkap keragaman genetik Durian Tengkurak menggunakan penanda ISSR.
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<i>The Durian Tengkurak (Durio tanjungpurensis Navia) is one of the endangered exotic species in the Malvaceae family. The species is important for conservation of the germplasm and is considered a potential genetic resource for the development of durian in the future. The objective of this research project was to assess the molecular diversity of D. tanjungpurensis in West Kalimantan, based on Inter Simple Sequence Repeat (ISSR) markers. We applied ten ISSR primers to reveal the genetic diversity of 60 individuals from six natural endemic D. tanjungpurensis populations. The genetic diversity parameters were estimated based on binary data about PCR products (present or absent bands). The results showed that the mean number of observed alleles, the mean number of effective alleles, the genetic diversity, the Shannon?s Information Index score, the number of polymorphic loci, and the percentage of polymorphic loci were 1.53, 1.29, 0.17, 0.26, 77.83, and 52.59, respectively. An analysis of molecular variance (AMOVA) showed that the genetic diversity within a population (65%) was higher than that found between the populations (35%). UPGMA clustering and principal coordinate analysis, based on the DICE similarity matrix, were used to classify the populations into three groups: 1) Hutan Rejunak and Tembaga, 2) Bukit Merindang, and 3) Hutan Rawak, Bukit Sagu 1, and Bukit Sagu 2. Further analysis of the population structure using STRUCTURE software was used to classify all the individuals into two major categories, thus uniting Groups 2 and 3 as one major category. In conclusion, a high level of genetic diversity in the Durian Tengkurak was revealed utilizing the

ISSR markers employed in the study.</i>