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HASIL PENILAIAN SEJAWAT SEBIDANG ATAU PEER REVIEW
KARYA ILMIAH : JURNAL ILMIAH**

Judul Jurnal Ilmiah (Artikel) : Identifikasi Molekuler Jeruk Nipis Tegal Berdasarkan Fragmen Gen 18s Ribosomal RNA
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 (jika ada)
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Nilai pengusul = (40% x 24,61) = 9,844				9,844

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Semarang, 27 April 2023

Reviewer I



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c. Kecukupan dan kemutakhiran data /informasi dan metodologi (30%)		7,50		7,50
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Semarang, 28 April 2023

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**SSR MARKERS CHARACTERIZATION FOR TEMU IRENG (*Curcuma aeruginosa* Roxb.) GENERATED FROM EST OF *Curcuma longa*****Karakterisasi Marka SSR untuk Temu Ireng (*Curcuma aeruginosa* Roxb.) dari EST *Curcuma longa*****Devit Purwoko^{1*}, Siti Zulaeha¹, Teuku Tajuddin¹, Hayat Khairiyah¹, Reynaldi Zulfikar Fauzi², Priyanti²**¹Laboratory for Biotechnology OR-PPT BRIN, 630 Building, Puspiptek Area, Tangerang Selatan, Banten 15314, Indonesia²Program Studi Biologi, Fakultas Sains dan Teknologi, Universitas Islam Negeri Syarif Hidayatullah, Jl. Ir. H. Juanda No 95, Ciputat Timur, Tangerang Selatan, Banten 15412, **Indonesia***Email: devit.purwoko@bppt.go.id**ABSTRACT**

Temu ireng (Curcuma aeruginosa) is used as a traditional herb medicine in Indonesia. Expressed Sequence Tags (EST) of C. longa was used because there were no genome data of C. aeruginosa. This study aimed to recognize the diversity of SSR characteristic and to develop a primer for C. aeruginosa genetic diversity. The EST was preprocessed and analyzed for the SSR motif. Primers were designed using SSR motifs excluding mononucleotide (≥ 20 bp) and analyzed based on gene ontology. The result showed that out of 12.675 EST used there were 3.005 contig and 548 perfect SSR motif with the motif frequency of 1/15,27 kb sequences achieved. AGG trinucleotide was mostly distributed (37,40%). There were 380 primers designed and 10 primers validated by PCR on three C. aeruginosa clones from Ponorogo, Cikarang, and Kebumen. The number of alleles detected was about 2 to 3 per locus. The polymorphic microsatellite markers produced from this study could be used for the analysis of genetic diversity of C. aeruginosa in Indonesia.

Keywords: *Curcuma aeruginosa*, *Curcuma longa*, EST, primer, SSR**ABSTRAK**

Temu ireng (*Curcuma aeruginosa*) digunakan sebagai bahan baku obat herbal tradisional di Indonesia. *Expressed Sequence Tags (EST)* dari *C. longa* digunakan karena sampai saat ini belum adanya data genome dari *C. aeruginosa*. Penelitian ini bertujuan untuk mengetahui keragaman karakteristik SSR dan mengembangkan primer untuk prastudi keragaman genetik *C. aeruginosa*. EST dilakukan prapemrosesan dan dianalisis motif SSR. Primer didesain menggunakan motif SSR selain mononukleotida (≥ 20 bp) dan dianalisis berdasarkan ontologi gen. Hasil yang diperoleh dari 12.678 EST yang digunakan dihasilkan 3.005 contig dan 548 motif perfect SSR dengan frekuensi motif 1/15,27 kb sekuen. AGG trinukleotida merupakan yang paling banyak terdistribusi (37,40%). Sebanyak 380 primer didesain dan 10 primer divalidasi melalui PCR pada 3 klon *C. aeruginosa* asal Ponorogo, Cikarang, dan Kebumen. Jumlah alel yang terdeteksi sekitar 2 sampai 3 per lokus. Marka mikrosatelit polimorfik yang dihasilkan dari penelitian ini dapat digunakan untuk analisis keragaman genetik *C. aeruginosa* di Indonesia.

Kata Kunci: *Curcuma aeruginosa*, *Curcuma longa*, EST, primer, SSR