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Resistensi Molekuler dan Filogenetik Cabai Katokkon (Capsicum sp. Katokkon) Berdasarkan Internal Transcribed Spacer dan Sequence Characterized Amplified Region Terpaut Gen Bs3
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RESISTENSI MOLEKULER DAN FILOGENETIK CABAI KATOKKON (*Capsicum* sp.'Katokkon') BERDASARKAN *INTERNAL TRANSCRIBED SPACER* DAN *SEQUENCE CHARACTERIZED AMPLIFIED REGION* TERPAUT GEN *Bs3*

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INTISARI

Cabai (*Capsicum* sp.) merupakan tanaman hortikultura bernilai ekonomi tinggi yang dibudidayakan secara luas di seluruh dunia, termasuk Indonesia. Salah satu ancaman dalam budidaya cabai adalah penyakit *bacterial spot* yang disebabkan oleh *Xanthomonas euvesicatoria* sehingga penggunaan kultivar yang membawa gen resistensi *Bs3* merupakan strategi pengendalian yang efektif. Namun, distribusi *Bs3* pada kultivar cabai lokal Indonesia belum banyak diketahui. Selain itu, identitas spesies spesifik cabai Katokkon secara molekuler belum dikonfirmasi dengan komprehensif. Penelitian ini bertujuan mendeteksi keberadaan *Bs3* pada 16 kultivar cabai menggunakan *marker SCAR PR-Bs3*, serta mengidentifikasi spesies spesifik cabai Katokkon berdasarkan *marker Internal Transcribed Spacer* (ITS). Metode identifikasi resistensi molekuler meliputi isolasi DNA dengan *Phytopure Kit,* uji kualitatif, uji kuantitatif, dan amplifikasi PCR. Sementara itu, metode untuk identifikasi spesies cabai Katokkon meliputi DNA *sequencing,* analisis konsensus sekuens dengan EPI2ME dan BLAST pada basis data NCBI GenBank, serta rekonstruksi pohon filogenetik, jarak genetik, dan variasi genetik menggunakan MEGA X dan DNAsp. Hasil amplifikasi *PR-Bs3* menunjukkan bahwa 16 kultivar mengalami kerentanan terhadap infeksi *bacterial spot.* Sekuensing nanopore menghasilkan sekuens konsensus ITS Katokkon sepanjang 680 bp. Analisis variasi genetik menunjukkan 251 *polymorphic sites,* rata-rata jarak genetik 1% terhadap seluruh sekuens *C. chinense*. Pohon filogenetik menempatkan Katokkon dalam satu *clade* yang sama dengan seluruh aksesi *C. chinense*.

Kata kunci: *Bacterial spot,* DNA *barcoding*, ITS, Katokkon

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MOLECULAR RESISTANCE AND PHYLOGENETIC OF KATOKKON PEPPER (*Capsicum* sp.'Katokkon') BASED ON INTERNAL TRANSCRIBED SPACER AND SEQUENCE CHARACTERIZED AMPLIFIED REGION LINKED TO THE *Bs3* GENE

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ABSTRACT

Chili peppers (*Capsicum* sp.) are horticultural crops of high economic value that are widely cultivated around the world, including in Indonesia. One of the threats to chili pepper cultivation is bacterial spot disease caused by *Xanthomonas euvesicatoria.* Therefore, the use of cultivars carrying the Bs3 resistance gene is an effective control strategy. However, the distribution of the Bs3 gene in local Indonesian chili pepper cultivars remains largely unknown. Furthermore, the molecular specific species identity of Katokkon pepper has not yet been comprehensively confirmed. This study aims to detect the presence of the Bs3 gene in 16 chili cultivars using the SCAR PR-Bs3 marker, as well as to identify specific species of Katokkon pepper based on the Internal Transcribed Spacer (ITS) marker. Methods for molecular resistance identification include DNA isolation using the Phytopure Kit, qualitative testing, quantitative testing, and PCR amplification. Meanwhile, methods for identifying the Katokkon pepper species included DNA sequencing, consensus sequence analysis using EPI2ME and BLAST against the NCBI GenBank database, as well as phylogenetic tree reconstruction, genetic distance, and genetic variation analysis using MEGA X and DNAsp. PR-Bs3 amplification results indicated that all 16 cultivars were susceptible to bacterial spot infection. Nanopore sequencing yielded a 680 bp Katokkon ITS consensus sequence. Analysis genetic variation at 251 polymorphic sites, with averages intraspecific genetic distances of 1% relative to the entire *C. chinense* sequence. The phylogenetic tree placed Katokkon in the same clade as all *C. chinense* accessions.

Keywords: Bacterial spot, DNA barcoding, ITS, Katokkon