



## **KARAKTERISASI GENOM KLOROPLAS TEBU (*Saccharum* 'Bululawang')**

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### **INTISARI**

Tebu (*Saccharum* spp.) merupakan komoditas strategis dalam industri gula nasional, sehingga pengembangan varietas unggul memerlukan dukungan informasi genetik yang akurat. Genom kloroplas berperan penting dalam proses fotosintesis dan metabolisme energi serta bersifat relatif konservatif, sehingga banyak dimanfaatkan dalam studi komparatif dan pemuliaan tanaman. Tebu 'Bululawang' ('BL') merupakan salah satu kultivar unggul yang luas dibudidayakan di Indonesia, tetapi informasi genom kloroplasnya masih terbatas. Penelitian ini bertujuan untuk mengkarakterisasi genom kloroplas tebu 'BL', menganalisis distribusi dan tipe motif *Simple Sequence Repeats* (SSR) kloroplas serta pola bias penggunaan kodon (*Relative Synonymous Codon Usage/RSCU*), dan membandingkan variasi genom kloroplas 'BL' dengan spesies pembanding berdasarkan *alignment* sekuens genom kloroplas. Genom kloroplas tebu 'BL' diperoleh melalui *Whole Genome Sequencing* (WGS) *long-read* menggunakan platform Oxford Nanopore Technologies (ONT) PromethION, diikuti perakitan, anotasi, serta analisis bioinformatika komparatif. Hasil penelitian menunjukkan bahwa genom kloroplas BL memiliki panjang sekitar 142,5 kb dengan struktur kuadripartit lengkap yang terdiri atas wilayah *Large Single Copy* (LSC), *Small Single Copy* (SSC), dan dua *Inverted Repeat* (IR), serta komposisi dan susunan gen yang konservatif. SSR kloroplas didominasi oleh motif mononukleotida dengan kecenderungan basa A/T, dan analisis RSCU menunjukkan dominasi kodon berakhiran A/T. Analisis *alignment* menunjukkan tingkat kesamaan sekuens yang tinggi pada wilayah pengode protein dan IR dibandingkan wilayah non-pengode. Penelitian ini menyimpulkan bahwa genom kloroplas tebu 'BL' bersifat konservatif, dengan variasi utama pada wilayah non-pengode, dan berpotensi dimanfaatkan sebagai referensi dalam studi komparatif dan pemuliaan tebu berbasis molekuler.

**KATA KUNCI:** Bululawang, genom, kloroplas, sekuensing, tebu



## **CHLOROPLAST GENOME CHARACTERIZATION OF SUGARCANE (*Saccharum* 'Bululawang')**

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### **ABSTRACT**

Sugarcane (*Saccharum* spp.) is a strategic commodity in the national sugar industry, therefore the development of superior varieties requires support from accurate genetic information. The chloroplast genome plays an essential role in photosynthesis and energy metabolism and is relatively conserved, making it widely utilized in comparative studies and plant breeding. Sugarcane 'Bululawang' ('BL') is one of the elite cultivars extensively cultivated in Indonesia; however, information on its chloroplast genome remains limited. This study aimed to characterize the chloroplast genome of sugarcane 'BL', to analyze the distribution and motif types of chloroplast Simple Sequence Repeats (SSR) as well as codon usage bias patterns (Relative Synonymous Codon Usage/RSCU), and to compare chloroplast genome variation in 'BL' with reference species based on chloroplast genome sequence alignment. The sugarcane 'BL' chloroplast genome was obtained through long-read Whole Genome Sequencing (WGS) using the Oxford Nanopore Technologies (ONT) PromethION platform, followed by genome assembly, annotation, and comparative bioinformatic analyses. The results showed that the BL chloroplast genome is approximately 142.5 kb in length and exhibits a complete quadripartite structure consisting of a Large Single Copy (LSC) region, a Small Single Copy (SSC) region, and two Inverted Repeats (IR), with a conserved gene composition and organization. Chloroplast SSRs were dominated by mononucleotide motifs with a strong A/T bias, and RSCU analysis revealed a predominance of codons ending in A/T. Sequence alignment analysis indicated a high level of sequence similarity in protein-coding regions and IRs compared with non-coding regions. This study concludes that the chloroplast genome of sugarcane 'BL' is highly conserved, with major variation occurring in non-coding regions, and has potential utility as a reference for comparative studies and molecular-based sugarcane breeding.

**KEYWORDS:** Bululawang, chloroplast, genome, sequencing, sugarcane