ANALISIS LEVEL EKSPRESI GEN *SPS*, *Sus1*, DAN *Sut1* PADA DAUN MUDA JAGUNG LADANG DAN JAGUNG MANIS (*Zea mays* L.) MENGGUNAKAN RT-qPCR

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INTISARI

Studi level ekspresi gen penyintesis sukrosa (*SPS*, *Sus1*, dan *Sut1*) pada daun muda jagung manis dan jagung ladang dilakukan untuk memahami mekanisme keseimbangan sukrosa yang terjadi di daun pada level transkrip karena berkaitan dengan kemampuan daun menyediakan dan mengekspor sukrosa ke jaringan lubuk. SPS mengubah UDP-glucose (UDP-G) dan fructose-6-phosphate menjadi sucrose-6-phosphate. Sus1 secara dapat balik (*reversible*) mengkatalisis pemecahan sukrosa dan menyintesis ulang sukrosa, dan Sut1 berperan sebagai kanal transportasi sukrosa menuju floem. Primer didesain menggunakan NCBI Primer BLAST untuk enam gen referensi (ACT, EF1 α, α-TUB, CYP, UBQ, dan GAPDH) dan tiga gen target (SPS, Sus1, dan Sut1). Dari optimasi primer didapatkan empat kandidat gen yang menunjukkan amplifikasi spesifik (ACT, ATUB, CYP, dan EF1A), dan dari seleksi stabilitas gen referensi menggunakan RefFinder, ACT adalah kandidat yang paling stabil sehingga bisa digunakan untuk normalisasi data gen target. Pada gen target, hanya Sus1 yang berhasil memunculkan pita spesifik, sementara SPS dan Sut1 mengamplifikasi non-target. Dalam penelitian ini, primer SPS dari *Saccharum officinarum* (SoSPS) yang sebelumnya sudah divalidasi secara in silico ditemukan juga pada sekuens gen SPS jagung, digunakan untuk mengkuantifikasi level ekspresi gen SPS jagung. Dari kuantifikasi relatif Livak, level ekspresi gen SPS paling tinggi dijumpai pada jagung manis sh2-op (42 kali Pertiwi 6), dan paling rendah pada Pertiwi 6 (jagung ladang). Sebaliknya, level ekspresi Sus1 paling tinggi pada Pertiwi 6 dan paling rendah di sh2-op (0,44 kali Pertiwi 6).

Kata kunci: *delta delta Cq, jagung manis, level ekspresi gen, RT-qPCR, sukrosa*

ANALYSIS OF EXPRESSION LEVELS OF *SPS*, *Sus1*, AND *Sut1* GENES IN FIELD CORN AND SWEET CORN (*Zea mays* L.) YOUNG LEAVES USING RT-qPCR

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ABSTRACT

The study of gene expression levels related to sucrose biosynthesis (SPS, Sus1, and Sut1) in young leaves of sweet corn and field corn was conducted to understand the mechanism of sucrose balance in the leaves at the transcript level, as it is related to the ability of leaves to supply and export sucrose to sink tissues. SPS converts UDP-glucose (UDP-G) and fructose-6-phosphate into sucrose-6-phosphate. Sus1 reversibly catalyzes the breakdown of sucrose and the resynthesis of sucrose, while Sut1 functions as a sucrose transport channel to the phloem. Primers were designed using NCBI Primer BLAST for six reference gene candidates (ACT, EF1α, α-TUB, CYP, UBQ, and GAPDH) and three target genes (SPS, Sus1, and Sut1). After primer optimization, four gene candidates showed specific amplification (ACT, ATUB, CYP, and EF1α), and the study of reference gene stability using RefFinder suggested ACT as the most stable reference gene so that it could be used for target gene data normalization. For target genes, only Sus1 showed specific bands, while SPS and Sut1 amplified non-target bands. In this study, SPS primers from *Saccharum officinarum* (SoSPS), which had been previously validated in silico, were also found in the corn SPS gene sequence, was used to quantify the expression levels of the maize SPS gene. Based on Livak relative quantification, the highest expression level of the SPS gene was found in sh2-op (42 times that of Pertiwi 6), and the lowest in Pertiwi 6 (field corn). In contrast, the highest expression level of Sus1 was found in Pertiwi 6 and the lowest in sh2-op (0.44 times that of Pertiwi 6).

Keywords: *delta delta Cq, gene expression levels, RT-qPCR, sucrose, sweet corn*