COMPARATIVE ANALYSIS OF MOLECULAR BIOLOGICAL MARKERS OF DIFFERENT SWEET CORN (ZEA MAYS L. CONVAR. SACCHARATA KOERN) GENOTYPES

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The leaf and crop samples required for our examination were collected from the campus of the Faculty of Agricultural and Food Sciences and Enviremental Managment of the University of Debrecen from the beginning of July to the end of July at 5 times. In our study we aim to follow the molecular biological markers of lutein biosynthesis by targeted gene expression studies in three sweet maize varieties: Dessert R78, Messenger and Honey during the generative phase of the plants. Quantitative real-time PCR (qPCR) is an effective tool for measuring gene expression levels at first, reliable reference genes will be identified for data normalization. During the sample collection to preserve the RNA replicates were collected and frozen immediately in liquid nitrogen and then stored at -80 °C until analysis.Previously we selected four reference genes for our studies, which encode tubulin (TUB), ubiquitin (UBI), actin (ACT) and a thioredoxin-like gene (TLG). From these four candidate reference genes three (TUB, UBI,ACT) gave satisfactory results and selected for further downstream studies. The PCR products have also been confirmed by sequencing and sequence alignment to respective genes. For lutein biosynthesis gene expression, 7 target genes and 8 pairs of primers were selected for preliminary studies (PSY,HYD,CYP97C,PDS,ZDS,LCYB,LCYE). These indicated that all real-time PCR reactions are suitable for further studies in our selection of sweet corn varieties.