

عنوان مقاله:

Differential gene expression analysis in high oil and low oil maize (zea mays) using RNA-seq data

محل انتشار:

چهارمین کنگره بین المللی و شانزدهمین کنگره ملی ژنتیک (سال: 1399)

تعداد صفحات اصل مقاله: 2

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خلاصه مقاله:

Background and Aim: Corn is one of the most important cereals grown in the world and is a major source of energy, protein and other nutrients for humans and livestock. Corn oil is a valuable corn product that is beneficial for heart health because of its unsaturated fats and Today it has a special place in human nutrition. Corn with more than ۶% oil called high-oil corn. In this study, two low-oil and high-oil maize cultivars were analyzed for differentiation gene expression. The aim of this research was to study gene expression profiles and to determine the marker genes in maize oil content. Methods: The raw data used in this study was included ۳ replicates for each treatment (high-oil and low-oil) from leaf tissue transcriptome (۴۰ days after pollination). After initial data processing, transcriptome of two treatments formed and arranged through alignment and locating the RNA-Seq reads on the maize reference genome (version BY۳_RefGen_v۴). then Differential gene expression analysis was performed. Results: finally ۵۷۰۶۳ gene and ۱۸۹۶ isoform on The genomes of these samples were identified. Between them recognized ۲۶۵۸ Significant differentially expressed genes with "p value < ۰.۰۰۵" and "log₂FC < ۲". Conclusion: Differences in gene expression can lead to different phenotypes in different species, so by identifying these genes, the origin of the relevant phenotype can be identified. Even today, the best technique for detecting gene expression differences is the RNAseq technique. Therefore, in this experiment, using RNA-seq technique, genes involved in corn oil production were identified

کلمات کلیدی:

corn oil , differential gene expression , transcriptome , RNA-seq

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