

عنوان مقاله:

Deciphering the Regulatory Network of Some Key Drought-responsive Genes and microRNAs in Canola

محل انتشار:

مجله منابع ژنتیک, دوره 10, شماره 1 (سال: 1403)

تعداد صفحات اصل مقاله: 11

نویسندگان:

Maryam Pasandideh Arjmand - Department of Plant Biotechnology, Faculty of Agricultural Sciences, University of Guilan, Rasht, Iran

Naser Farrokhi - Department of Cell and Molecular Biology, Faculty of Life Sciences and Biotechnology, Shahid Beheshti University, Tehran, Iran

Habibollah Samizadeh Lahiji - Department of Plant Biotechnology, Faculty of Agricultural Sciences, University of Guilan, Rasht, Iran

Mohammad Mohsenzadeh Golfazani - Department of Plant Biotechnology, Faculty of Agricultural Sciences, University of Guilan, Rasht, Iran

خلاصه مقاله:

Drought is a major abiotic stress that constrains the growth and yield of Canola. This study was conducted to obtain a greater insight into the drought-related hub genes, their regulatory network and relative expression pattern in tolerant and susceptible genotypes of Canola under drought stress. In present study, we sought to find some of key genes and their regulatory network involved in drought stress in Canola, and analyzed gene network, functional pathways, regulatory microRNAs (miRNAs) based on RNA-sequencing data analysis and comparing the relative expression pattern of hub genes in tolerant and susceptible genotypes by Real-time PCR technique. A total of 5275 differentially expressed genes were identified, with 3794 up-regulated and 1481 down-regulated genes under drought stress. The result showed that the most significant biological process of up-regulated and down-regulated genes enriched in response to water deprivation and light stimulus, respectively. The result demonstrated that the ACP4, RCA, FNR1, HCEF1, PRK, GDC, and MDH were some of hub genes in drought stress. The hub genes were regulated by vital drought-responsive miRNAs such as miR955a, miR854, miR172, miR834, miR390, and miR167. The relative expression pattern of investigated hub genes was different in tolerant and susceptible genotypes of Canola. The identified drought-responsive hub genes appear to play an essential role in the regulation of carbon metabolism, activation of stress signaling, and the regulation of the stromal NADP(H) redox state in response to drought stress. They are regulated by important miRNAs in a complex regulatory network that worth being considered in genetic engineering programs of Canola.

کلمات کلیدی:

miRNAs, PPI network, Real-Time PCR, RNA-Seq

لینک ثابت مقاله در پایگاه سیویلیکا:

<https://civilica.com/doc/2057322>

