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Pathways and co-expression network analysis of immune-related genes in short-term calorie restricted miceNehir Ozdemir Ozgenturk¹, Zehra Omeroglu Ulu¹, Soner Dogan², Bilge Guvenc Tuna² and Salih Ulu¹¹Yildiz Technical University, Davutpasa Campus, Turkey²Yeditepe University, Turkey

RNA-seq technology was performed by using a comparative transcriptome analysis of the MMTV-TGF- α female mice thymus tissues that were fed *ad libitum* (AL), chronic calorie restriction (CCR) (85% of AL fed mice) and intermittent calorie restriction (ICR) (3 weeks AL fed, 1 week 40% of AL fed mice) from 10 weeks of age to 17 weeks of age or 18 weeks of age. The results of RNA-seq analysis, a total of 6091 significantly differentially expressed genes (DEGs) were identified. 2821, 2825 and 445 significantly DEGs were detected between AL-CCR, CCR-ICR and AL-ICR fed groups, respectively. These DEGs were classified according to cellular components, biological processes and molecular functions Gene Ontology (GO) main categories. 188 of 2821, 36 of 445, 176 of 2825 genes were identified to be involved in immune system process (GO:0002376) biological processes GO categories. KEGG pathway and the gene co-expression network analysis between AL-CCR, CCR-ICR and AL-ICR fed groups immune-related DEGs were done using String database. For network analysis, nodes and edges presented the interaction between immune-related DEGs.

Biography

Nehir Ozdemir Ozgenturk completed her Graduation at Ege University; Master's degree in Plant Breeding department and; PhD in Department of Justus Liebig University. In 2003, she worked at Cereal Research Center in Canada as a Post doc. Also she worked at Georgia Medical School for four months with Nato fellowship. She has scientific paper in various scientific journals, publications and presentations at international conferences.

nehirozdemir@yahoo.com