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**Comparison of the effect of caloric restriction types on the expression of some cancer-associated genes via RNA-seq**Nehir Ozdemir Ozgenturk<sup>1</sup>, Ali Yasir Kaç<sup>1</sup>, Zehra Omeroglu Ulu<sup>1</sup>, Soner Dogan<sup>2</sup>, Bilge Guvenc Tuna<sup>2</sup> and Salih Ulu<sup>1</sup><sup>1</sup>Yildiz Technical University, Davutpasa Campus, Turkey<sup>2</sup>Yeditepe University, Turkey

Pathways and Co-expression Network Analysis of Immune-Related Genes in Short-term Calorie Restricted Mice RNA-seq technology was performed a comparative transcriptome analysis of the MMTV-TGF- $\alpha$  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 were presented the interaction between immune-related DEGs. Calorie restriction is to reduce the amount of calorie received without malnutrition. This manipulation method has positive effects on life span, cancer formation and immune response in the long run. However, there are also some systems such as lymph organs that respond quickly to lack of calories. Thymus is one of these lymph organs. In this study, two type calorie restriction practices (CCR/ICR) were used on MMTV-TGF- $\alpha$  transgenic mice and a group of mice were fed *ad libitum* (AL) as a control group. It is aimed to determine the changes that the nutrition type will bring about in the expression of genes. The manipulation started at the 10th week of the life of the mice and ended at the 17th and 18th week. RNA-Seq-based transcriptome were performed to the RNAs obtained from the thymus of the sacrificed mice. Through RNA-Seq results "Differential Expressed Genes" (DEGs) were determined. 6091 of them have been identified as statistically significant ( $p < 0.05$ ). The AKT1, CTCF, PTEN genes known to cause breast tumor development were selected by data banks. The selected genes were searched in three different RNA-Seq data and expression levels were determined for three genes in three different medium. Changes in expression level are displayed via graphics.

**Biography**

Nehir Ozdemir Ozgenturk completed her Graduation at Ege University; Master's Degree in Plant Breeding Department and PhD in the Department of Justus Liebig University. In 2003, she worked at the 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

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