Nehir Ozdemir Ozgenturk et.al., Hereditary Genet Curr Res 2018, Volume 7
DOI: 10.4172/2161-1041-C2-005

Effects of aging and calorie restriction on gene expression profiles

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There is evidence that Calorie Restriction (CR) retards aging and extends median and maximal life span. In this study, RNA-Seq was performed from MMTV-TGF-α mice thymus tissue which was performed short-term Ad Libitum (AL), Chronic Calorie Restriction (CCR) and Intermittent Calorie Restriction (ICR) feeding patterns. Based on the GO analysis in the MGI, genes related to aging and oxidative stress were identified and gene expression profiles were investigated in AL, CCR and ICR data. In our RNA-Seq data, 150 genes were detected from 292 genes related to aging in the MGI data, while 300 of 380 genes from MGI data related to oxidative stress were detected. The gene expression difference between these three data was found to be significant. When we compare 150 gene expression levels of 292 genes related to aging from MGI data, it was found that the genes related to aging in AL, CCR and ICR RNA-Seq data had quite different expression levels between AL and CCR, CCR and ICR, but similar between AL and ICR. 300 of the 380 genes associated with oxidative stress, the gene expression in the CCR data was mostly different from the gene expression in AL and ICR data.

Biography

Nehir Ozdemir Ozgenturk has completed her PhD from Justus Liebieg Universitaet. She is currently working in Yildiz Technical University as an Associate Professor.

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