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Overexpression of *Gclc* in the *Drosophila melanogaster* thorax

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Motivation and Aim: The enhancement of glutathione biosynthetic capability can determine longevity and delay aging. Our recent studies demonstrated that *Gclc* overexpression slows down the age-dependent decline of locomotor activity and circadian rhythmicity without effect on fecundity [1]. Here we analyzed the effects of neuronal *Gclc* overexpression in the thorax of *Drosophila melanogaster* on the transcriptomic changes.
Methods and Algorithms: Transcriptomic analysis was performed using control UAS-Gclc flies and flies with *Gclc* overexpression at the age of 1 (young), 4 (matured) and 6 weeks (old). Processing of transcriptomic data was performed using PPLine toolkit [2] including read preprocessing (trimmomatic), mapping (STAR) and counting (HTSeq-count). The further analysis was done with R programming language (R core Team). The edgeR package was used for analysis of differential expression [3]. KEGG gene set enrichment analysis (GSEA) was performed using clusterProfiler [4].
Results: We derived RNA sequencing expression profiles for 12000 genes (after eliminating low expression ones). The expression of 760 genes (108 of 760 have FDR < 0.05) demonstrated association with *Gclc* overexpression in all of the groups: young/mature/old or males/females. When the selected threshold of expression was 2-fold or more (FDR < 0.05), *Gclc* overexpression down-regulated 42 genes and up-regulated 14 genes, such as *SMC2* (*Structural maintenance of chromosomes 2*), *w* (*white*), *CG4293*, *Gclc*, *Cyp4p2* (*cytochrome P450 4p2*), *Ipk1* (*Inositol-pentakisphosphate 2-kinase*), *CG8157*, *CR45457*. The *Gclc* level demonstrated associations with expression of genes involved in a variety of cellular processes.
Conclusion: Transcriptome analysis of the thorax of Gclc transgenic flies revealed pathways that may contribute to the longevity and prevent the age-dependent decline of biological functions.
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