

Meta-analysis of the heat shock response of *Drosophila melanogaster*

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Motivation and Aim: More than 30 years ago, existence of a unified response to different stressors in insects was found in *Drosophila*. Then its neurohormonal mechanism was described and characterized by high conservatism [1, 2]. With the development of sequencing and data analysis technologies, it has become possible to reconstruct and predict genetic mechanisms more precisely. Based on the analysis of the transcriptomic response to heat shock, we aim to reconstruct the stress response system in more details.

Methods and Algorithms: In meta-analysis of transcriptomic data, we used Python3 scripts that are partially based on InterTransViewer [3] program. Functional annotation of genes was performed by using NCBI, Ensembl, FlyBase databases and the ShinyGO v0.77 [4] utility. Gene network reconstruction was made by using StringDB database.

Results: We found only three heat shock experiments in *D. melanogaster* conducted in the same conditions [5, 6]. Due to the low number of experiments, we decided not to use the formula for calculating weights proposed by the InterTransViewer program and to focus on differentially expressed genes with a standard level of confidence ($FDR \leq 0.05$). A total of 235 genes common among 3 data sets were found. Four major groups of genes were identified: those involved in lipid catabolism, protein stacking, translation regulation in response to stress, and – unexpectedly – in response to cold.

Conclusion: Through the use of functional annotation of the selected genes and analysis of additional literature, we expanded the existing gene network of response to heat shock. However, additional experimental verification of the results obtained is required.

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