TRANSCRIPTOMIC RESPONSE OF *DROSOPHILA MELANOGASTER* TO ARSENITE EXPOSURE

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Nowadays, arsenic and its compounds find wide applications as alloying agents across various industrial sectors, including glass processing, pigment manufacturing, textile production, papermaking, and metallurgy. Additionally, arsenic is utilized in the formulation of pesticides, food additives, and pharmaceuticals[1]. The chemical industry continues to produce an increasing number of inorganic arsenic compounds to facilitate diverse production processes. This raises the question: Are these chemicals long-term safe for humans and the overall condition of an ecosystem?

It is evident that every chemical containing arsenic, whether organic or inorganic, should undergo biological safety testing. However, conducting tests on mammals for each new compound is time-consuming and, to some extent, ethically challenging. Therefore, it is suggested that general assessments could be conducted using smaller and simpler organisms such as *Drosophila melanogaster*.

This research aimed to determine the transcriptomic response of fruit flies to arsenite exposure. Six experimental groups (male and female) were subjected to varying concentrations of arsenious oxide (0 mM, 0.25 mM, and 1 mM) by adding it to their nutrient medium. It also contained basic ingredients such as agar and maize powder, sugar, dried yeast, Nipagin, and propionic acid [2]. RNA samples were collected after 0 hours (for control groups), 1 hour, 8 hours, and 24 hours by extracting them from flies' heads [3]. The expression profiling was obtained by next-sequencing technology with Illumina NextSeq 550. The raw data in BCL file format was processed in a complex bioinformatics pipeline. It included such tools as SRA Toolkit [4], hisat2 [5], samtools [6], featureCounts, and DESeq2 [7]. Finally, differential expression heatmaps were obtained. They, together with survival rate data, allowed us to draw some conclusions about specific protective pathways against arsenic compound intoxication.

The results of the experiment have demonstrated that arsenic toxicity profoundly alters normal cellular mechanisms. Transcriptome analysis showed that the arsenic response might be divided into two conditional phases. The early stage included active expression of genes involved in arsenic resistance and oxidative stress pathways; chaperone genes were also affected, indicating deregulation of protein synthesis by arsenic exposure as well. The late phase of response was characterized by a more specific response to stress, as arsenic metabolism pathways were activated. Survival rate data suggested that the most important steps of the response to intoxication take place in the first hour of exposure. It was also noted that female flies tended to have a higher survival rate (73% against 7% at 0.25 mM and 56% against 0% at 1 mM). Thus, it was concluded that *Drosophila melanogaster* likely has protective pathways associated with sex. While

there were some substantial differences between the transcriptomic responses of male and female flies, no sex-specific mechanisms were detected due to insufficient existing gene ontology information. Arsenic intoxication significantly influences transcriptomic mechanisms in approximately 70 genes, with one-fifth of them still belonging to the uncategorized group.

References:

1. HUGHES, M., BECK, B., CHEN, YU Arsenic Exposure and Toxicology: A Historical Perspective. În: *Toxicological sciences*, 2011, vol. 123, pp. 305-332
2. LAKHOTIA, S., RANGANATH H. *Experiments with Drosophila for Biology Courses.* Banglore: Indian Academy of Sciences, 2021, 634 p.
3. HEMPHILL, W., RIVERA, O., TALBERT, M. RNA-sequencing of Drosophila melanogaster head tissue on high-sugar and high-fat diets. În: G3: Genes, Genomes, Genetics, 2018, vol. 8, pp. 279-290
4. Github NCBI SRA Toolkit Documentation [citat 13 martie 2024]. Disponibil: https://github.com/ncbi/sra-tools/wiki
5. Github Pages HISAT2 Manual [citat 13 martie 2024]. Disponibil: https://daehwankimlab.github.io/hisat2/manual/
6. HtslibSamtools Manual [citat 13 martie 2024] Disponibil: https://www.htslib.org/doc/samtools.html
7. Bioconductor: Analyzing RNA-seq data with DESeq2, © Michael I. Love, Simon Anders, and Wolfgang Huber 2024 [citat 14 martie 2024]. Disponibil: https://www.bioconductor.org/packages/release/bioc/vignettes/DESeq2/inst/doc/DESeq2.html

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