EVALUATION OF THE ARSENIC EFFECTS ON C. ELEGANS MODEL SYSTEM

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Arsenic is a highly toxic element that can be found in the environment. Particularly its presence in food composites is a serious risk for both humans and animals. The main source of exposure is arsenic-contaminated groundwater used in agriculture to irrigate crops, which could potentially lead arsenic entering in food chain. Epidemiologic studies have shown a significant association between the consumption of arsenic through drinking water and cancers of the skin, lung, bladder, liver, and kidney, neurologic disease, cardiovascular disease, as well as other non-malignant diseases. There are several techniques for assessing changes in gene expression: the DNA microarray and, most recently, the study of MicroRNA (miRNAs) for the detection of early indicators in various diseases. MiRNAs are a novel class of small noncoding RNAs that modulate the expression of genes at the post-transcriptional level. These small molecules have been shown to be involved in cancer, apoptosis, and cell metabolism. In vivo studies were performed in C.elegans model system in order to evaluate arsenic effect on microRNA profiles. We investigated changes in miRNA expression profiles in C.elegans at two different time-points (6 and 24 hours) after exposure at different concentrations of sodium arsenite (0, 0.1, 0.5 mM). At first, we focused our attention to some miRNA families homologous to humans. Preliminary results show an effect of arsenic on the profiles of miRNA expression; in particular we observed an up-regulation of some microRNAs such as lin-4 (mir125 counterpart in humans), let-7 (human homologue let 7, d, e, a, i, b), mir57 (mir-100, mir-99 counterpart in human), mir-234 (human homologue mir-137), which were found to be up-regulated in some conditions of stress as reported in a recent study of Simone et al, 2009. The up-regulation of these microRNAs, caused by the treatment with sodium arsenite, could confirm the hypothesis that the oxidative stress underlies the mechanism of exposure to this xenobiotic, and that miRNAs play an important role on cellular response to genotoxic oxidative stress.

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