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Short Communication

Environmentally Relevant Concentrations of Human Exposure to the Arsenic Anhydride and Manifested in the Proteomics Technology

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ABOUT THE STUDY

Humans are most exposed to arsenic through the consumption of arsenic-contaminated food and water. Until recently, the major focus of attention was only on drinking arsenic-contaminated groundwater and human health. However, because groundwater is utilized primarily for agriculture irrigation, an increase in arsenic content in agricultural soils and agronomic products was expected. Furthermore, because straw and husk are commonly used as animal feed, arsenic is deposited in the bodies of birds and animals through feed. As a result,humans are exposed to arsenic poisoning due to arsenic consumption by eating the animal foods such as beef, mutton, hog, chicken, egg, milk,and fish etc. Furthermore, fish or many aquatic species are naturally harmed because they feed, reproduce, and develop in polluted aquatic habitats, exposing them to contaminants for the rest of their lives. As a result, in addition to other sources, fish and other aquatic foods can contribute to total dietary arsenic intake by people, potentially increasing human health risks [1].

The zebra fish (*Danio rerio*), as well as various other non-model fish species, have been utilized to investigate the molecular pathways behind arsenicosis pathophysiology. Zebrafish contribute significantly to the understand the mechanisms of arsenic poisoning. Arsenic has been demonstrated in studies to interfere with immunological function, resulting in immune suppression. The impact of arsenic poisoning in zebra fish and other aqua cultured species has been investigated using genomics methods. In human medicine, the development of prognostic and diagnostic biomarkers for arsenicosis would be critical. Fish models have made a significant contribution to understanding the toxicological and pathophysiology of arsenicosis, which may eventually aid in identifying solutions to the environmental concern [2].

Omics methodologies have been used to explore a variety of complicated diseases in order to better understand their causes and mechanisms, as well as to generate prognostic and diagnostic biomarkers. Toxicity is the study of the interaction of ecosystems, chemical contaminants, and biological creatures. It is based on the concept that chemical pollution may have hazardous consequences on individuals and populations of organisms. Traditionally, impacts were discovered using biomarkers, which were almost always substances or processes that were known to be impacted by pollution. Proteomics allows for high-throughput investigation of impacts on protein populations and subpopulations, potentially leading to the discovery of new biomarkers. Toxic proteomics is being used to study a wide range of toxicants, including pharmaceuticals, natural compounds, metals, industrial chemicals, nanoparticles, and nanofibers. It has also been used to address challenges at several levels, ranging from the identification of toxicants principal molecular targets to the understanding of the molecular reactions of cells and tissues to toxicants. Proteomics research has already revealed the mechanisms of action of a variety of chemicals, ranging from metals to peroxisome proliferators. As we move towards the post-genomic age, new correlations between proteins and toxic pathological consequences are continually being discovered, and tremendous development is on the horizon [3].

In arsenic-exposed species, proteomics technology has been utilized to identify toxicity pathways, detoxification routes, protein-interacting network maps, and biological response .Over the last decade, there has been a tremendous shift in the environmental sciences toward the use of high-throughput molecular tools capable of detecting simultaneous changes in hundreds, if not thousands, of molecules and molecular components after organisms are exposed to various environmental stressors. These omics approaches have gotten a lot of interest because they have the potential to not only uncover novel mechanisms of physiological and toxic action, but also to find biomarkers of exposure and consequences in fish and aquatic invertebrates [4].

Rapid innovations in genomics and proteomics have given researchers the tools they need to look into how arsenic exposure impacts global gene and protein expression. Differential gene

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expression in the livers of zebra fish exposed to sodium arsenite at dosages up to 500 ppb for 7 days was discovered using a combination of proteomic and transcriptome analysis, which revealed reduced mRNA levels of genes involved in cell cycle and lipid metabolism. Differential expression of proteins related with lipid transport and metabolic pathways was observed at lower concentrations (50 ppb) of sodium arsenite and one isoform of apolipoprotein is one of them, which is an important biomarker, utilized in fibro test [5].

CONCLUSION

Previous proteomic explorations focused primarily on gel electrophoresis combined with tandem Mass Spectrometry Analysis (MSA), and Zebrafish proteomes for embryonic stages, liver, and lens were described. The number of proteins discovered is small, ranging from a few hundred to several thousand. Liquid Chromatography (LC) has been more popular in the last five years for protein separation prior to Mass Spectrometry Analysis. Zebrafish proteomes for lungs, cerebellum, nucleus accumbens, tail, muscle fibers, and other organs have been described using this method. The new method has discovered thousands of proteins, ranging from few more hundred to over four thousand. In recent years, there has been a growing tendency to use zebrafish for developmental analysis, clinical research, and chemical toxicity evaluations.

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