Assessing radiobiological effects of low doses of ionizing radiation on zebrafish muscle by two-dimensional gel electrophoresis

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Introduction: This work relates with the application of zebrafish - Danio rerio - to the study of radiobiological effects of low doses of ionizing radiation. In recent years, the use of zebrafish has grown considerably, pointing more and more as a very interesting model in biomedical research, essentially because of the level of homology shared with the human genome, complemented by an easy and reasonably affordable practical side. The two-dimensional gel electrophoresis (2DGE) is a method used for the analysis of complex protein mixtures from biological samples. This method allows the detection of differences in protein expression under different conditions, so allowing creating relations between those differences and the irradiations that were in their basis. The present work aimed at evaluating proteome changes in the zebrafish muscle caused by low doses of X-rays exposure.

Material and Methods: Animals were externally irradiated with three distinct dose protocols (100 mGy, 500 mGy and 1.000 mGy). One day after the irradiation, the animals were sacrificed and a muscle sample was collected. 2DGE was then used to identify proteins that showed a differential expression after X-rays exposure.

Results: About 85 ± 21 protein spots were identified in every gel. The statistical analysis of protein expression recognized differences between the control and the irradiated groups (27 spots to 1000 mGy; 22 spots to 500 mGy; 3 spots to 100 mGy). Most differentially expressed proteins were downregulated in irradiated groups when compared to the control group.

Conclusions: The present work seems to confirm that the 2DGE based methodology might be considered as an adequate analytical tool for study radiobiological effects at the molecular level in zebrafish. It has been found that a large number of proteins were downregulated, suggesting that a remodelling of the muscle proteome occurs

after the exposition to low doses of X-rays. Mass spectrometry analysis should be performed in order to allow the identification of those proteins that were affected by exposition to ionizing radiation. This identification would most probably contribute for a deeper insight concerning the metabolic and physiological consequences of the exposition to X-ray.

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