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Proteomic analysis by SILAC and 2D-DIGE reveals radiation-induced endothelial response: Four key pathways

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Epidemiological data show that ionising radiation increases the risk of cardiovascular disease. The endothelium is one of the main targets of radiation-induced damage. Rapid radiation-induced alterations in the biological processes were investigated after exposure to a clinically relevant radiation dose (2.5 Gy gamma radiation). The changes in protein expression were determined using the human endothelial cell line EA.hy926 as a model.

Two complementary proteomic approaches, SILAC (Stable Isotope Labelling with Amino acids in Cell culture) and 2D-DIGE (Two Dimensional Difference-in-Gel-Electrophoresis) were used. The proteomes of the endothelial cells were analysed 4 h and 24 h after irradiation. Differentially expressed proteins were identified and quantified by MALDI-TOF/TOF and LTQ Orbitrap tandem mass spectrometry.

The deregulated proteins were mainly categorised in four key pathways: (i) glycolysis/ gluconeogenesis and synthesis/degradation of ketone bodies, (ii) oxidative phosphorylation, (iii) Rho-mediated cell motility and (iv) non-homologous end joining. We suggest that these alterations facilitate the repair processes needed to overcome the stress caused by irradiation and are indicative of the vascular damage leading to radiation-induced cardio- and cerebrovascular impairment.

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