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Epigenetic changes in human fibroblasts after low dose rate γ radiation

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Recently, the epigenetic mechanisms involved in cancer development have come in focus. An epigenetic event refers to changes in gene expression controlled by histone modifications (acethylation) and/or DNA methylation (gene silencing). Accumulated evidence indicates that epigenetic modifications including persistent proteomic changes are among the delayed effects of ionizing radiation (IR). It has been suggested that radiation induced genome instability and transgeneration effects may be epigenetically mediated. Understanding the epigenetic mechanisms related to low dose and low dose rate radiation may also provide valuable information with significant implications in radiation protection and cancer prevention. To investigate the protein expression profile and identify the modified proteins, we have performed 2D-PAGE analysis in primary human fibroblast cells (VH10) after exposure to IR at low dose rate.

In the present study, human fibroblast cells were exposed to 1 Gy of gamma radiation delivered at 4.1 mGy/h. To investigate the late effect of IR, cells were sub-cultured and repeatedly collected from 3 hours up to 28 days post-irradiation. 2D-PAGE analysis was performed on cells collected at 3h, 7 and 28 days post-irradiation to study the proteomic changes.

Our preliminary results based on analysis of 2D-PAGE gels by PD-Quest software indicate that changes in protein expression can be observed at least 28 days post-irradiation. Notably, most of the modified proteins at 28 days post-irradiation were down regulated.

Further, the results on protein profiles at different post exposure times and proteins sequenced by mass spectrometry will be presented.

Primary author: Ms SHAKERI MANESH, Sara (Stockholm University)

Co-authors: Prof. WOJCIK, Andrzej (Stockholm University); Prof. HARMS-RINGDAHL, Mats (Stockholm University); Mrs SKIÖLD, Sara (Stockholm University); Dr HAGHDOOST, Siamak (Stockholm University)

Presenter: Ms SHAKERI MANESH, Sara (Stockholm University)

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