Does gene expression analysis allow the discrimination of radiation qualities?

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Gene expression analysis was carried out in human T-lymphoma Jurkat cells in order to identify robust candidate genes showing significant gene expression alterations after exposure to I-123-iododeoxyuridine, γ-rays and α-particles.

Equi-effect radiation doses, i.e. radiation doses and exposure conditions causing the same biological effect level, were determined with regard to micronucleus formation, γ-H2AX foci signal intensity and apoptosis induction after γ-irradiation (Cs-137, 0.7 Gy/min), α-irradiation (Am-241, 0.032 Gy/min) and exposure to the Auger electron emitter I-123 as I-123-iododeoxyuridine (I-123-UdR). I-123-UdR was incorporated into the DNA for 20 h. Absorbed radiation dose was assessed based on accumulated decays, point-kernel calculations and the 3-D morphology of the cells. Gene expression analysis was performed employing whole human genome DNA-microarrays (Agilent) after exposure to equi-effect radiation doses. RNA for gene expression analysis was isolated 6 and 24 h post-exposure. Potential candidate genes for the discrimination of radiation quality have to show a significant expression change (>1.5 fold; $p < 0.05$) and display no altered gene regulation or even a conversely regulation in response to exposure to the other radiation qualities investigated. Gene expression of selected candidate genes was validated via qRT-PCR. Biological processes and pathways of significantly regulated genes were subsequently analyzed.

At equi-effect doses 359, 598 and 1339 genes were significantly regulated after exposure to I-123-UdR, α-particles and γ-rays, respectively. Applying the above described requirements for candidate genes, we identified 4, 1 and 1 gene(s) allowing the reliable and robust discrimination between γ- vs. I-123-UdR-exposure, γ- vs. α-radiation and α- vs. I-123-UdR-exposure, respectively.

The results indicate that the discrimination of different radiation qualities by means of gene expression is possible.