Rearrangements in human chromosome 1 visualized by arm-specific probes in the progeny of blood lymphocytes exposed to iron ions

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It is well known that heavy ions are more effective than sparsely ionizing radiation in the induction of chromosomal aberrations in heavy ions. However, most of the complex rearrangements induced by densely ionizing radiation ultimately lead to cell death. For risk assessment, it is more important to measure the residual cytotgenetic damage in cells surviving the exposure and able to proliferate. This analyses will be strongly influenced by the technique used to visualize the chromosomes, and consequently on the aberrations scored. For instance, symmetrical exchanges have higher transmission probability than asymmetrical exchanges. Multi-fuor FISH (including mBAND, mFISH, or RxFISH) allows the detection of many different aberrations with high resolution, but it is slow and expensive, thus affecting the statistical power of the study. In this study, we hybridized metaphase cells with human DNA probes specific for the p and q arms of the chromosome 1. The arm-specific probes allow a fast and reliable detection of both symmetrical and asymmetrical inter-chromosomal exchanges and inter-arm intra-changes in the painted chromosome pair. We used this method to score aberrations in human lymphocytes exposed to 1 Gy of either 250 kVp X-rays or 1 GeV/n Fe-ions (LET=145 keV/μm) and harvested following 120 h in culture, including 2 h in colcemid for metaphase-block. Although iron ions are much more effective than X-rays in the induction of chromosomal aberrations formed during the first post-exposure cell-cycle, we found that the effectiveness drops when daughter cells are scored at a late harvest time. The results will be discussed with the aim of identifying the aberrations relevant for late effects of heavy ions.