

COMPARISON M-FISH – FISH 3 PAINTING TECHNIQUES FOR LOW DOSES

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In the case of retrospective dosimetry, the detection of translocations is the most appropriate method. The development of Fluorescent In Situ Hybridization (FISH) techniques has allowed an easy detection of these stable aberrations. Two FISH techniques are available; with the FISH-3 painting (F3P) only three chromosomes are painting, while M-FISH allows the painting of all chromosomes with a specific colour. For F3P a specific calculation is used to extrapolate the number of translocations observed on three chromosomes to the genomic one, whereas with M-FISH all chromosome rearrangements are seen.

The aim of this presentation is therefore to compare the sensitivity of the two approaches. We therefore scored translocations in peripheral blood lymphocytes irradiated at different doses of gamma radiation (0; 0,1; 0,2; 0,3 and 0.5 Gy).

First of all, whatever the dose (0 to 0,5 Gy) the translocation frequencies were from 2 to 8 times higher with M-FISH than with F3P. The difference between the two techniques is that with M-FISH all rearrangements generated in the cell are observed, while F3P translocation frequencies is an extrapolation from what is detected on three chromosomes. Our results suggest that the extrapolation coefficient is not appropriate.

In addition, translocation frequencies generated after exposure to 0,1 and 0,2 Gy were not significantly different from the frequency observed at 0 Gy whatever the technique used. However, a significant difference between translocations frequencies is measured after exposure to 0,3 vs. 0 Gy with the M-FISH technique, while such a difference was not detected with the F3P technique. Therefore the M-FISH seems to be a more sensitive technique than the F3P.

The yield of translocations at 0,1 and 0,2 Gy is very low probably because the number of scored cells is not sufficient. However, increasing the cell number is time consuming particularly with the M-FISH technique.

In conclusion, the main advantage of M-FISH is the direct screening of the whole genome, so all chromosome rearrangement can be observed in one experiment and an eventual bias is avoided. Therefore, the applicability of M-FISH to retrospective biological dosimetry will be discussed.