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Abstracts



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An improved statistical methodology for analysis of translocations for biodosimetry purposes

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Introduction

Due to the "stable" nature of translocations within the lymphocyte population, the Fluorescence *in situ* Hybridisation (FISH) assay is a useful radiation biodosimetry method when the time period between exposure and dose assessment is large (Barquinero *et al.*, 2017). However, statistical analysis of these data is usually based on the dicentric assay method, leading to potentially incorrect results.

Methods

A data driven approach to analysis of observed excess radiation induced translocations has been carried out to facilitate estimation of radiation dose and the associated uncertainty following application of the FISH translocation assay. Classical assessment of the most suitable statistical model(s), a detailed consideration of the uncertainty budget and the minimum detectable dose, followed by a pragmatic approach to propagation of errors is proposed, resulting in development of a full ISO standard-compliant method (JCGM, 2008) or Bayesian alternative for biodosimetric analysis translocations.

Results

A review of the literature reveals that, in contrast to methods for detection and scoring of translocations, data analysis methods are not standardised within the active biodosimetry community. For example, some laboratories use their own age-matched control populations to adjust for the background signal and others make use of published data in the literature (Sigurdson *et al.*, 2007).

Data from a number of case studies will be presented with the results of the original analysis compared with the newly proposed method. The results depend on a number of factors, however, in most cases, the newly proposed rigorous method of statistical analysis results in a larger and likely more correct assessment of the uncertainty associated with the estimated dose.

Conclusion

The standard methodology for translocation analysis, based on transferring the methods from the much simpler dicentric assay, is in most cases not suitable for translocation assay. This is due to the larger range of uncertainties and the relatively large contribution to the uncertainty in dose from the age adjustment. The newly developed methodology presented here provides a pragmatic framework for calculation of dose and uncertainty using the FISH translocation assay, based on a precise consideration of the translocation data and experimental set up.

References

Barquinero JF *et al.* 2017. *Int J Radiat Biol.* 93:30-35. doi 10.1080/09553002.2016.1222092.

JCGM 100:2008. https://www.bipm.org/utis/common/documents/jcgm/JCGM_100_2008_E.pdf.

Sigurdson AJ *et al.* 2008. *Mutat Res.* 652:112-21. doi 10.1016/j.mrgentox.2008.01.005.

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