

The effect of Colcemid time on the length change dynamics of chromosomes: its importance for biodosimetry

Thiago de Salazar e Fernandes^{1, 3*}, David Lloyd², Ademir Amaral¹, Catão Temístocles Barbosa³ and Romildo de Albuquerque Nogueira³

¹ Grupo de Estudos em Radioproteção e Radioecologia – GERAR; Departamento de Energia Nuclear, UFPE; Av. Prof. Luiz Freire, 1000; 50740-540, Cidade Universitária, Recife, PE, Brazil.

² Health Protection Agency / Radiation Protection Division, Chilton, Didcot, OX11 0RQ, United Kingdom.

³ Grupo de Biofísica Teórica e Computacional; Departamento de Morfologia e Fisiologia Animal, UFRPE; Rua Dom Manuel de Medeiros, s/n; 52171-900, Dois Irmãos, Recife - PE.

* Author for correspondence: thiagosalazar@hotmail.com

ABSTRACT

Metaphase analysis for radiation induced chromosomal aberrations in human lymphocytes is a useful tool for biodosimetry. During mitosis chromosomes condense to a minimum length at metaphase, and some researchers suggest this process is non-linear and can be modified by the actions of some drugs and chemicals. The conventional method is to arrest cycling lymphocytes in metaphase by adding the spindle inhibitor Colcemid for the last 2 or 3h of in vitro culture. There are a number of advantages, which are discussed, for adding the drug earlier particularly when investigating partial body exposures. However, depending on the timing and concentration of the drug, excessive contraction of the chromosomes can occur so that aberration detection is difficult or impossible. This research investigated some problems of excessive contraction using human chromosomes # 2 and 3 highlighted for accurate identification by FISH. A computerised image analysis system was used to measure the lengths of the two pairs of chromosomes averaged over 50 metaphases from 72h cultures with Colcemid added at 0.05µg/mL either for the final 3h or 48h. The dynamical process of the transitional stage (length changes of chromosomes # 2 and 3 from 3 to 48h treatment with Colcemid) was evaluated by a non-linear method described by Peng et al. (1994) called Detrended Fluctuation Analysis (DFA). It was found that adding Colcemid earlier induced significantly greater condensation ($t > 1.98$; $p < 0.05$), and the dynamic process of the length changes of the transitional stage has a random-walk like behavior with scaling exponent (α) from DFA approximately 1.13 ± 0.05 ($n=4$). These results demonstrate that the transitional process of additional chromosome contraction from the longer Colcemid exposure is similar to a random event, but in fact it is not random and can be predictable, suggesting the existence of a deterministic chaotic state for the process of chromosome packing.

Keywords: Colcemid time treatment, chromosome contraction, nonlinear dynamics.