


Letter to Editor Re: Fang et al entitled “Assessment of Genomic Instability in Medical Workers Exposed to Chronic Low-Dose X-Rays in Northern China”

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With great concern, we read an article by Fang et al entitled “Assessment of Genomic Instability in Medical Workers Exposed to Chronic Low-Dose X-Rays in Northern China” recently published in the journal *Dose-Response*.¹ This is an important issue associated with radiation protection since the accurate assessment of health risks from such low-dose radiation remains challenging and controversial. However, the presentation and conclusion of this work are ambiguous. We focus our comments on the foremost limitation of the article by Fang et al¹ (ie, the analyses of cytogenetic data) that weakens their conclusion of a strong correlation between genomic instability and the duration of exposure to low-dose radiation. The use of working years to categorize the subjects is inappropriate and should not be used since there were large variations in exposure levels in each group of workers. A more accurate metric to relate biological damage to exposure is the level of radiation dose.

The authors used the analysis of variance (ANOVA) to test the interaction between smoking and chromosome aberrations and a Student *t* test to determine the differences in MN frequencies between groups. Nonetheless, the authors did not present the transformation method to normalize the raw cytogenetic data for achieving the reasonably homogeneous inter-variability within groups prior to statistical analyses.¹ This is one of the major drawbacks of their work since it has been well-established that the ANOVA and a Student *t* test are the proper statistics to be used with normal distribution data sets.^{2,3} However, cytogenetic data are not normal distribution but are Poisson distribution or overdispersion^{4,5} because many cells with no damage will be detected along with cells carrying damage. Hence, if the ANOVA and the Student *t* test will be used, the transformation procedure (eg, the square root transformation^{4,5} and the log transformation⁴) must be applied to the raw data prior to statistical analyses. If there is no data transformation, a likelihood of a false-positive result is increasing.^{2,6} Thus, the ANOVA and Student *t* test methods used by Fang *et al*¹ to

analyze the non-normal distribution cytogenetic data without transformation are inappropriate and might have led to their conclusion of the positive effects of low-dose radiation. Further, the scoring of only 100 metaphases per subject is insufficient to obtain tangible results for the detection of the true differences between groups within this dose range. The International Atomic Energy Commission has recommended at least 500 metaphases per subject be scored when dealing with radiation doses less than or equal to 1000 mSv.⁷ Additionally, the study was conducted in northern China where high levels of radon were reported,⁸ which may be another confounding factor relating to cytogenetic data. All the above information and the major scientific problems present in this letter indicate that there is little support for the conclusion that genomic instability is induced in medical workers exposed to low-dose radiation. Our review provides adequate information to reject the conclusions reached in the work presented by Fang et al.¹

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