Letter to the Editor
Diagnostic Genetics

Evaluating the Cumulative Impact of Ionizing Radiation Exposure With Diagnostic Genetics

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Dear Editor,

I have scrutinized the salient article by Jang et al. [1] with great interest. Using the most advanced cytogenetic dosimetry techniques, the authors successfully evaluated the in vitro damaging impact of ionizing radiation on human chromosomes. In particular, they examined the effects of single X-ray radiation exposure on cultured and stained lymphocytes isolated from peripheral blood samples of four non-smoking, healthy, Korean young adults. In general, this represents a remarkable advance and exciting primary exploration of the technique. Given increasing concerns related to the risks of ionizing radiation from medical diagnostic imaging raised by both the scientific community and public, I also have some comments on expanding the applications of this work to clinical investigations.

First, accumulating evidence points to the long-term carcinogenic effects of ionizing radiation on children, adolescents, and medical professionals. Amongst clinical diagnostic imaging modalities, X-rays, intra-operative imaging, and computed tomography (CT) have stochastic ionizing radiation effects [2]. Pearce et al. [2] analyzed the association of CT scans with malignant tumors among 178,604 patients <22 years old who received scans between 1985 and 2002, and found a positive association of leukemia and brain tumors with CT radiation dose. Another Australian-based study including 11 million subjects indicated an increased incidence of cancer after CT radiation exposure in children and adolescents [3]. According to the latest National Institute for Health and Care Excellence (NICE) guideline, CT and/or total body CT scanning are not recommended for children and adolescents below 16 years [4].

A representative example of radiation exposure in adolescents is the use of X-rays for patients with adolescent idiopathic scoliosis (AIS). Although the natural course of AIS is considered generally favorable without treatment, based on a 50-year follow-up study [5], common clinical practice involves regular monitoring with repetitive whole-spine X-rays [6]. However, increasing lines of evidence indicate increased cancer risks, especially breast cancer, for AIS patients after long-term follow up in various cohorts [7, 8].

Several medical specialists are subjected to regular radiation exposure, including nuclear medicine physicians, radiologists, orthopedic surgeons, and interventionists. Thus, there has been increasing interest on the effects of low-dose radiation for this population [9]. According to the U.S. Department of Energy, doses below 100 mGy are defined as low-dose radiation [10]. Accordingly, among the 11 X-ray single-dose points used by Jang et al. [1], only 0.05 Gy and 0.1 Gy belong to low-dose radiation. Given that clinical investigators are seeking to improve diagnostic imaging with low or zero radiation, the potential future application of the cytogenetic analysis proposed by Jang et al. [1] should be explored for...
such cumulative low-dose radiation detection.

Second, data derived from next-generation sequencing of the human genome are becoming increasingly available for clinicians and laboratory medicine professionals. Genomic mutations, including single-base and insertion/deletion variations, can now be readily identified with this technique. Human lymphocytes can be applied to both genomic sequencing and chromosomal aberrations. Therefore, it would also be interesting for Jang et al. [1] to expand their research to studying the relation between these two types of alterations.

Overall, Jang et al. [1] provide a valuable tool for investigating cytogenetic dosimetry by analyzing chromosomal morphological changes of peripheral lymphocytes from healthy adults. I further propose that this laboratory technique can be applied to clinical investigations, especially for evaluating the cumulative effects of low-dose radiation. For more profound studies, I also propose relating these findings to prevalent next-generation sequencing data.

Authors’ Disclosures of Potential Conflicts of Interest

There are no conflicts of interest to declare.

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