LETTER TO THE EDITOR


Armen K.Neressian

Laboratory of Carcinogenesis, Cancer Research Centre, 76 Fanardjian Street, Yerevan 75052, Armenia

Email: genetik@ysu.am

Dear Sir

I read with great interest the research findings of Dr. Rajeswari and co-workers (1). I draw attention to the extremely high background micronucleus (MN) level in exfoliated buccal mucosa cells of untreated cancer patients and their first degree female relatives (3.41 and 1.65%, respectively) compared with controls (0.27%). This means that in buccal cells of cancer patients and their relatives MN frequencies were 12.6- and 6.1-fold higher than in control subjects.

Analysis of some recent publications has shown that after exposure to environmental mutagens, such as pesticides (2), organic solvents and lead-containing pigments (3), radioactive iodine (4) and antineoplastic drugs (5), MN level increased only 2.7–3.7 times (2,3) or did not increase significantly (4,5).

It is extremely unlikely that the difference in MN content in the same healthy population may differ by 6.1 times (female relatives and controls) while after exposure to mutagens the differences between exposed subjects and controls were 2.7–3.7.

My opinion is supported by some recent papers concerning cytogenetic disturbances in lymphocytes of breast cancer patients and their female relatives (6,7). The differences in the levels of chromosomal aberrations in lymphocytes of patients and their relatives were 1.4 (6) and 1.7 (7) and between relatives and controls was 1.5 (6) (data concerning control subjects was not presented in Trivedi et al.; ref. 7). Moreover, a paper by Jyothish et al. (8) showed no differences (neither constitutional nor structural) in lymphocytes of breast cancer patients and their relatives compared with control subjects. However, it is well established that use of MN in exfoliated buccal mucosa cells to detect chromosomal damage induced by various mutagens is less efficient than that of both MN and chromosomal aberrations in lymphocytes (3,5). Thus, if the difference in chromosomal aberration levels in lymphocytes of relatives and control subjects is <2, the difference in MN level in buccal mucosa cells should be at least the same, but no more.

I suggest that the extremely high levels of cells with MN (1) were due to two causes. Rajeswari et al. (1) analyzed only 1000 cells from each subject, although for this purpose at least 3000–5000 (9) and even, in the opinion of Belien et al. (10), 10 000 exfoliated cells should be studied, due to a low baseline MN frequency. The second reason may be the use of Giemsa staining instead of DNA-specific stains (acridine orange, Hoechst 33258 plus pyronin, propidium iodine or DAPI) because the latter can eliminate most of the artefacts associated with use of DNA non-specific stains (9).

In conclusion, I suggest that, along with real MN, Rajeswari et al. (1) registered artefacts due to the few cells scored and the use of Giemsa staining.

References


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Abbreviation: MN, micronucleus.