LETTERS TO THE EDITOR

Mobile Phone Radiation and Gene Expression
Dariusz Leszczynski
STUK—Radiation and Nuclear Safety Authority, Helsinki, Finland

Two studies (1, 2) in which the authors examined the effects of mobile phone radiation on gene expression using the transcriptomics approach were published in the June 2006 issue of Radiation Research. Both studies concluded that there is no effect of mobile phone radiation on gene expression because the number of statistically significantly affected genes was lower than the expected number of false positives. This conclusion seems to be premature.

In both studies, the authors examined gene expression in cells exposed either to mobile phone radiation or to a stimulus known to alter gene expression (positive control). As stated in both papers, the mobile phone radiation and the positive control stimuli caused statistically significant changes in gene expression. However, in the case of the positive control stimuli, the number of statistically significantly affected genes was higher than the expected number of false positives, but for mobile phone radiation the number of affected genes was lower than the expected number of false positives.

In both papers, the authors did not show lists of the genes whose expression was statistically significantly affected by the mobile phone radiation. However, in both articles the genes whose expression was statistically significantly affected by the positive control stimuli were shown in tables, even though the authors had no ability to distinguish which of the genes were indeed affected and which were the false positives.

The genes affected by mobile phone radiation were not shown in either study, presumably because all of them were considered as false responses. However, the observation that the number of affected genes was lower than the number of expected false positives does not automatically mean that every gene appearing as affected by mobile phone radiation is a false positive. This calculation (the number of expected false positives) shows the probability that the affected genes might be false positives, but it does not mean that all of them are indeed false positives.

In a similar study published in 2004 in Proteomics, we analyzed changes in protein expression in cells of a human endothelial cell line using a proteomics approach (3). The number of statistically significantly affected proteins detected in our samples was lower than the expected number of false positives. However, further analysis of one of the affected proteins, vimentin, has shown that this protein did respond to the mobile phone radiation. Therefore, even though the number of statistically significantly affected proteins was lower than the expected number of false positives among these affected proteins, we found a protein that was indeed affected when we used other methods of analysis.

Therefore, the conclusions of the authors of both studies (1, 2) that mobile phone radiation has no effect on gene expression are premature and are not supported by the experimental evidence presented. The authors should show which genes were statistically significantly affected by the mobile phone radiation and then determine whether these were indeed false positives by using other, non-transcriptomic, methods.

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References


Reply to the Comments by Leszczynski on “Mobile Phone Radiation and Gene Expression” by Qutob et al.

James P. McNamee,* Sami S. Qutob,* Vinita Chauhan* and Andrew Williams*
“Consumer and Clinical Radiation Protection Bureau and Biostatistics and Epidemiology Bureau, Healthy Environments and Consumer Safety Branch, Health Canada

This letter is in response to comments by Dariusz Leszczynski concerning two recently published studies in Radiation Research (1, 2). In this commentary, Dr. Leszczynski argues that both studies suffer from flaws in the statistical methodologies in relation to false discovery rates (FDR). Specifically, Dr. Leszczynski states that both studies have (a) shown that “mobile phone radiation and the positive control stimuli caused statistically significant changes in gene expression”, (b) not shown “lists of the genes whose expression was statistically significantly affected by mobile phone radiation . . . presumably because all of them were considered as false positives”, and (c) not used other “non-transcriptomic methods” to determine whether “statistically significant genes were indeed false positives.” Based on the above concerns, Dr Leszczynski states that the two studies have prematurely come to the conclusion that mobile phone radiation has no effect on gene expression without support from strong experimental evidence.

We would first like to emphasize that Dr. Leszczynski appears to have grouped comments that may be relevant for the study conducted by Whitehead et al. (2) with those of our study (1). It must be noted that the two studies were conducted quite differently in terms both of experimental design and statistical analysis. The experimental design employed in our study involved five independent experiments with six conditions per experiment, resulting in 30 independent hybridizations on nonpoled RNA. Under these conditions, a relatively large number of independent biological replicates presumably reduced the probability of false-positive events resulting from chance and/or slight differences in culture conditions (3). Furthermore, the application of the James-Stein shrinkage test for the estimator of the error variance in our study also minimized the generation of false positives or negatives that can occur when a common variance is assumed (4). However, it must be clearly stated that MAA-NOVA did not indicate any statistically significant changes in the expression of genes in the mobile phone radiation treatment groups relative to the sham control. As such, no differentially expressed genes were disregarded on the basis of the expected number of false positives. Furthermore, RT-PCR analysis of several heat-shock proteins validated our microarray results. Therefore, the comments by Dr. Leszczynski do not appear to be relevant to our study.

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