

CHANGES IN GENE EXPRESSION PROFILE OF MCF-7 CELLS AFTER EXPOSURE TO ELF MF AND RF EMF

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BACKGROUND: Up to the present, there have been many studies indicating that gene expression could be altered by EMF exposure, but most of them focused on single gene, and contradictory data still remain in the literature. The high-throughput screening techniques (HTST) have been proposed as a useful approach to determine all the possible biological effects of environmental stress on biological systems, e.g., microarray-based transcriptomic analysis allows researchers to evaluate globe-gene expression changes induced by exogenous stimulus.

OBJECTIVE: To investigate the global change of gene expression pattern induced by 50 Hz or 1800 MHz electromagnetic fields in breast cancer cell line MCF-7 cells, and identify key EMF-responsive genes.

METHODS: MCF-7 cells were exposed to 50 Hz 0.4 mT magnetic fields [1], or 1800 MHz EMF at 3.5 W/kg of time-averaged SAR for 24 hours. Total RNAs were isolated by Trizol method and then purified by using QIAGEN⁻s RNeasy mini Kit. Affymetrix Genome U133A gene chips (2 chips for control and 2 for exposure) were applied to detect the gene expression pattern following the manufacturer⁻s instruction. Data was analyzed by Affymetrix microarray suite version 5.0 (MAS 5.0) and Affymetrix Data Mining Tool 3.0 (DMT 3.0).

RESULT: MAS 5.0 software analysis showed that there were more than 1,000 differentially expressed genes. Among them, reproduction and coincidence analyses with DMT 3.0 software revealed that 30 genes were affected by ELF MF exposure with 100% consistency in 4 pairwise comparisons, including 6 down-regulated and 24 up-regulated genes. Gene clustering analysis was carried out to predict the function-unknown responsive genes.

The same procedure was applied to analyze genes affected by RF EMF, and 5 up-regulated genes were found after exposure to RF EMF for 24 hours at 3.5 W/kg of time-averaged SAR, including protein phosphatase 1 regulatory (inhibitor) subunit 12A (PPP1R12A), transducin (beta)-like 1X-linked (TBL1X), ephrin-B2 (EFNB2), topoisomerase (DNA) I (TOP1) and a function unknown gene.

CONCLUSION: ELF MF exposure may induce differential gene expression in MCF-7 cells, however, this cell line seems be not so sensitive to RF EMF exposure. Generally, the displayed change of expression level is small. The applicability of HTST needs to be discussed, and a set of manipulation and judgement standards is required.

[1] G.L. Hu, H. Chiang, Q.L. Zeng, and Y.D. FU. ELF Magnetic Field Inhibits Gap Junctional Intercellular Communication and Induces Hyperphosphorylation of Connexin43 in NIH3T3 Cells. *Bioelectromagnetics*, Vol. 22, pp. 568-573, 2001.

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