



Investigation of gene expression alterations in human peripheral blood cells after continuous wave exposure at 900 MHz

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Interactions between electromagnetic fields and biological tissue have been investigated multiple times in the past in epidemiologic studies (e.g. [1]) or exposure tests (e.g. [2] for *in vitro*, or [3] for *in vivo* tests), yet until now the only harmful effect that has been identified by reproducible, well designed experiments is the thermal damage by overheating. Hence, statutory thresholds for radio frequency electromagnetic fields (RF-EMF) have been established in order to limit relevant heat supply in human tissue, measured via the specific absorption rate (SAR). Although non-thermal biological effects are believed to be much weaker, new versions of microarrays (8x60k v2) allow for a more detailed detection of even non-coding RNAs and are hoped to display different adaptive processes in cells after irradiation.

In an *ex vivo* study, peripheral blood cells from 5 donors were exposed to a RF-EMF continuous wave of 900 MHz for 0, 30, 60 and 90 min [4]. Additional samples were either SHAM exposed or treated with a temperature of 2°C over room temperature (RT+2°C). Significant gene expression changes which show in addition at least a 2-fold change with respect to the SHAM exposed samples were identified by microarray analysis. The data were finally compared with data from the RT+2°C samples. While an open TEM waveguide was used for the experiments, other exposure environments (e.g. electromagnetic reverberation chambers and micro TEM cells) were considered, and their advantages and restrictions will be discussed.

To be able to relate biological observations to the radiation dose, a rigorous SAR dosimetry has been performed based on the measured temperature rise of the samples during the irradiation. To this end, temperature values captured by a thermography camera have been related to the corresponding SAR via a physical model of the transient power balance inside the samples.

In total 521 significantly deregulated transcripts were detected in all RF-EMF exposed groups relative to the SHAM exposed samples. Moreover, these transcripts were not expressed in their corresponding RT+2°C controls. An attempt to verify these indications by microarray data-based bioinformatics approaches, including enrichment and network analyses administered to expressed gene subset profiles, failed to identify the targeted biological response. Correspondingly, 14 candidate transcripts examined by qRT-PCR revealed an absence of correlation with respect to the microarray results.

As an intermediate conclusion, we find that 900 MHz EMF exposure to whole blood cells at a SAR between 7.2 and 13.3 W/kg induces no detectable alterations in gene expression during short-time exposure until 90 min [4]. Future investigations will include more donors and an optimized exposure setup for additional results.

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[2] Herrala, M., Mustafa, E., Naarala, J., Juutilainen, J.: Assessment of genotoxicity and genomic instability in rat primary astrocytes exposed to 872 MHz radiofrequency radiation and chemicals, *International Journal of Radiation Biology*, Vol. 94, No. 10, pp. 883-889, 2018.

[3] Akdag, M., Dasdag, D., Canturk, F., Akdag M. Z.: Exposure to non-ionizing electromagnetic fields emitted from mobile phones induced DNA damage in human ear canal hair follicle cells, *Electromagnetic Biology and Medicine*, Vol. 37, No. 2, pp. 66-75, 2018.

[4] Lamkowski, A., Kreitlow, M., Radunz, J., Willenbockel, M., Sabath, F., Schuhn, W., Stiemer, M., Fichte, L. O., Dudzinski, M., Böhmelt, S., Ullmann, R., Majewski, M., Franchini, V., Eder, S., Rump, A., Port, M., Abend, M.: Gene Expression Analysis in Human Peripheral Blood Cells after 900 MHz RF-EMF Short-Term Exposure. *Radiation Research* 189(5), pp. 529-540, 2018.