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Brain proteome response following whole body exposure of mice to mobile phone or wireless DECT base radiation

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The objective of this study was to investigate the effects of two sources of electromagnetic fields (EMFs) on the proteome of cerebellum, hippocampus, and frontal lobe in Balb/c mice following long-term whole body irradiation. Three equally divided groups of animals (6 animals/group) were used; the first group was exposed to a typical mobile phone, at a SAR level range of 0.17–0.37 W/kg for 3 h daily for 8 months, the second group was exposed to a wireless DECT base (Digital Enhanced Cordless Telecommunications/Telephone) at a SAR level range of 0.012–0.028 W/kg for 8 h/day also for 8 months and the third group comprised the sham-exposed animals. Comparative proteomics analysis revealed that long-term irradiation from both EMF sources altered significantly ($p < 0.05$) the expression of 143 proteins in total (as low as 0.003 fold downregulation up to 114 fold overexpression). Several neural function related proteins (i.e., Glial Fibrillary Acidic Protein (GFAP), Alpha-synuclein, Glia Maturation Factor beta (GMF), and apolipoprotein E (apoE)), heat shock proteins, and cytoskeletal proteins (i.e., Neurofilaments and tropomodulin) are included in this list as well as proteins of the brain metabolism (i.e., Aspartate aminotransferase, Glutamate dehydrogenase) to nearly all brain regions studied. Western blot analysis on selected proteins confirmed the proteomics data. The observed protein expression changes may be related to brain plasticity alterations, indicative of oxidative stress in the nervous

Authors' contributions: AFF and LHM conceived the concept and design of the experiments, made the literature survey and the final biologically valid interpretation of the EMF impact upon the brain, wrote and finalized the manuscript. AFF carried out all animal handling, welfare, EMF exposure, part of brain dissection and immunoassays. AS performed the brain dissection and brain regions' separation, contributed to the non-EMF writing of the manuscript and together with MHA, EK and EA carried out a part of the immunoassays and contributed to the data evaluation related to neuroproteomics. AX, AP and KV were involved in 2-DE experiments, Maldi ToF/MS, protein identification and statistical analysis. DJS participated in the conception of the design and contributed to the interpretation and evaluation of the overall data. GThT participated in the experimental design and experimental protocols optimization, coordinated the proteomics study, carried out the overall differential proteomics analysis and data evaluation and contributed to the proteomics writing of the manuscript. All authors read and approved the final manuscript.

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