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Effects of radiofrequency field from 5G communication on fecal microbiome and metabolome profiles in mice

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Abstract

With the rapid development of 5G networks, the influence of the radiofrequency field (RF) generated from 5G communication equipment on human health is drawing increasing attention in public. The study aimed at assessing the effects of long-term exposure to 4.9 GHz (one of the working frequencies of 5G communication) RF field on fecal microbiome and metabolome profiles in adult male C57BL/6 mice. The animals were divided into Sham group and radiofrequency group (RF group). For RF group, the mice were whole body exposed to 4.9 GHz RF field for three weeks, 1 h/d, at average power density (PD) of 50 W/m^2. After RF exposure, the mice fecal samples were collected to detect gut microorganisms and metabolites by 16S rRNA gene sequencing and LC–MS method, respectively. The results showed that intestinal microbial compositions were altered in RF group, as evidenced by reduced microbial diversity and changed microbial community distribution. Metabolomics profiling identified 258 significantly differentially abundant metabolites in RF group, 57 of which can be classified to Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways. Besides, functional correlation analysis showed that changes in gut microbiota genera were significantly correlated with changes in fecal metabolites. In summary, the results suggested that altered gut microbiota and metabolic profile are associated with 4.9 GHz radiofrequency exposure.