

## YEAST ADAPTIVE RESPONSE TO THE VERY HIGH-FREQUENCY ELECTROMAGNETIC RADIATION

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**Background.** The question of the influence of the very high frequency (VHF) electromagnetic radiation on living organisms is still under discussion.

**Aim.** The **aim** of the presented study was to determine the effects of VHF electromagnetic exposure on *Saccharomyces cerevisiae* strains and evaluate their possible adaptive response to the stress factor.

**Methods.** For this purpose, molecular-genetic analysis at the genomic and transcriptomic levels was carried out. *Saccharomyces cerevisiae* haploid and diploid strains were treated by VHF electromagnetic radiation and cultivated in YPD media supplemented with agar for 7 days. Genome variability was detected using PCR with primer to tetranucleotide repeat and the relative expression level of genes encoding the ubiquitin-conjugating enzyme (UBC6), two enzymes of fatty acids synthesis (OLE1 and FAS1), and two flocullins (FLO1 and FLO11) was defined by RT-PCR. Characteristics for both haploid and diploid strains were registered at three-time points: immediately, 24 hours and, 7 days after exposure.

**Results.** Comparative analysis of amplicon patterns obtained by amplification with primer to short repeat revealed differences in nucleotide sequences in haploid strain only immediately after irradiation. The sets of PCR-fragments of control and exposed samples after 7 days were identical. Results of comparative analysis of genes expression between non-irradiated and irradiated *S. cerevisiae* strains showed that there were no changes immediately after exposure and a slight decrease of genes expression up to 2 times was detected at 24 hours and 7 days after exposure although the increase of expression level of all analyzed genes was observed at 7th day after irradiation.

**Conclusions.** The results obtained in our research suggest that VHF electromagnetic irradiation can cause genome rearrangement in *S. cerevisiae* haploid strain reflecting possible repair processes but the major changes occur at the gene expression level supposing epigenomic regulation of adaptive process in yeast.