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ABSTRACTS

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BIOINFORMATIC SEARCH OF THE NONCODING GENOME FUNCTIONAL ELEMENTS OF GENES UP-REGULATED IN RESPONSE TO OXIDATIVE STRESS

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This study focuses on bioinformatics search for new regulatory structures in the non-coding DNA, located around the patterns of gene expression levels changed significantly in response to oxidative stress. The expression patterns activated in response to the low dose of oxidative stress (0.2 MPa, 1 h) in the brain of newborn rats were revealed. The study of genes up-regulated in response to oxidative stress were carried out on the DNA array (Affimetrix). We hypothesized that all genes with increased expression in response to oxidative stress may have the same motifs in non-coding DNA. To search motifs we've created an integrated collection database of transcription binding sites - JASPAR, TRANSFAC, Hocomoco TF Homo sapiens, Uniprobe TF Mus musculus. Two types of regulatory regions, the promoter region and the sequences with the capture of potential cis-regulatory modules were studied. The results of analysis demonstrated that the promoter regions of genes that are overexpressed in response to oxidative stress are enriched with binding sites for SOX transcription factor family. In contrast, genes non-responsive to oxidative stress mainly bear binding sites for HX (A, B, C, D) transcription factor family.

These data allowed hypothesizing about the interaction of the coding and noncoding elements of the genome in response to oxidative stress. The study was supported by Russian Ministry of Science and Education, grant №6.703.2014/K.