

Microarray detection of highly expressed genes in peripheral blood mononuclear leukocytes from patients with chronic ethanol intoxication

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Objective. Peripheral blood mononuclear leukocytes (PBMC) are the most accessible material for gene expression screening studies. According to international genetic databases (BioGPS, GeneAtlas U133A) most of drugs and xenobiotic detoxification genes have very low basal level of expression in PBMC. Nevertheless, a number of genes have a similar expression profile in blood cells and hepatocytes, which has a certain diagnostic potential.

Materials and methods. Using diagnostic chips Drug Metabolis Arrayit Pathways™ Focused and Human Discover Chips™ were used to identify the most intensely expressed genes of detoxification xenobiotic, ethanol and drug metabolism in cDNA mixes from healthy volunteers (n = 4), and patients with chronic ethanol intoxication (n = 8) compared to HeLa cell culture cDNA and multitissue cDNA mix ArrayIT Universal reference Cy3-labeled cDNA™. MEV 4.8.1 and Expander 6 software packages were used for microarray results analysis.

Results. In PBMC of chronic ethanol intoxication patients and HeLa cells culture revealed increased spots fluorescence corresponding to microsomal glutathione transferase 1 (MGST1) and muscle pyruvate kinase (PKM2) genes: MGST1> PKM2 for of chronic ethanol intoxication and, conversely, PKM2> MGST1 for HeLa

cDNA. In multitissue cDNA mix the most highly intense had genes associated with detoxification of arsenic derivatives and metabolism of sterols and fatty acids. The most variable (Up regulated) among all samples proved the gene for cytochrome P450 family 2, C polypeptide 8 (CYP2C8).

Conclusions. Microarray screening designed for gene selection and future implement more precise methods. For RT-PCR study of detoxification processes and chronic ethanol intoxication this revealed genes can be considered as the most probable markers for variations of expression in peripheral blood mononuclear leukocytes.

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