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with 10%FBS. To simulate hypoxia model, cardiomyocytes were plated in hypoxia chamber (1%O_2, 5%CO_2, 94%N_2) for 3, 6, 12, 24 h and the control group was incubated in normal conditions (5%CO_2, 95%O_2). Cell viability was determined using MTT-assay. Annexin-V assay was used to monitor apoptosis. Gene expression profiling was analysed with Affymetrix-HG-U133-Plus-2 arrays. Following bioinformatic and statistical analyses differentially expressed genes (DEG) were classified according to gene ontology using DAVID and KEGG pathway analysis tools.

According to MTT, Annexin-V and HIF gene expression results, hypoxia time was determined as 3 h. We identified 649 genes (279 down-regulated and 370 up-regulated) ($P < 0.001$, Fold change ≥1.5) were differentially expressed in hypoxic-AC16 vs. AC16. DEGs were mainly clustered in cell proliferation, regulation of cell death, cell adhesion and response to stress. Furthermore, transcriptome analyses revealed that 'Metabolic, cytokine-cytokine receptor interaction, HIF-1 signaling, TGF-beta, cell cycle and apoptosis' pathways were involved in the hypoxic stress response of human cardiomyocytes.

This study provides molecular information regarding gene expression reprogramming of human myocardial hypoxia. The pathways identified in this study may pave the road for translational medicine. This study was supported by TUBİTAK project number 111S189.

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Angiogenic potential of endothelial progenitor cells derived from induced pluripotent stem cells

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Autologous iPS cells after reprogrammed into endothelial progenitor cells (EPCs) may offer several advantages in the treatment of cardiovascular disorders because of their cardiogenic and vasculogenic differentiation potential. To reach that purpose, we differentiated and characterized mouse iPS cells into $Flk1^+$, a well-recognized EPC marker. Further maturation of EPC was derived from iPS cells and these cells have vascular formation and angiogenic potential in 3D culture. EPC drived iPS cells play important role in the treatment of cardiovascular disease.

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Electrophysiological, biochemical and genotoxic effects of Luna Experience on heart tissue in rat model

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Pesticides are widely used for the control of agricultural, industrial and domestic pests. However, the uncontrolled use of pesticides has diverse effects on ecological system and public health. Fungicides are one of the pesticide type used to kill fungi or fungal spores. In this study, the effect of different doses of Luna Experience, a fungicide, on the cardiac electrophysiology and genotoxicity in rats were investigated. Among five groups (5 mg, 10 mg, 20 mg, control and positive control for comet assay) treatment groups received by gavage doses of Luna Experience for 30 days. Electrical activity of heart were recorded using electrophysiological recording techniques. Tissue activities of paraoxanase (PON) and arylesterase (ARE) and level of malondialdehyde (MDA) were measured using biochemical methods. Comet assay was performed on heart tissue. We calculated genetic damage index (GDI) and damaged cell percent (DCP) from comet assay. It was observed that there is a significant decrease in heart rate in all treated groups as compared with control group ($P < 0.05$). Amplitude of P wave and QRS complex did not change ($P > 0.05$). In all treated groups, statistically significant differences were found for values of PON, ARE, MDA, GDI and DCP when compared to control group ($P < 0.05$). According to our results, exposure to different doses Luna Experience have a probable hazard potential for the cardiac system.