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THE REGULATION OF TRANSCRIPTION EFFICIENCY IN MICE' DIFFERENT CELL TYPES UNDER 37-DAY SPACEFLIGHT AT US ISS

Abstract

The investigation of biomaterial, fixated under weghtlessness conditions let us unique possibility to determine strategy of finding protective methods for human under long-term space flight and sybsequent readaptation for gravity of Earth and, possibly, Mars. The purpose of this work was to evaluate the mRNA content of the genes encoding cytoskeletal proteins in cardiomyocytes and lung tissue cells, total methylation level and its regulation in mice that had been euthanized on the board of the US Segment of the International Space Station 37 days after the start of the SpaceX-4 spacecraft (September 2014, USA). Four study groups were separated out: the flight group (F), the group of the ground synchronous control (G), vivarium control group (V), basal control group (B). In turn, relative content of mRNA of genes encoding beta-, gamma-actin, actin-binding proteins, beta-tubulin in cardiomyocytes was similar in all the study groups. Des, Actn4, Cct5, Cct7, Cycs, Gapdh mRNA content in the flight group F decreased compared to the group G. In the lung tissue cells the relative mRNA content in the flight group decreased for Actb, Des, Svil, Actn4, Cct7, Cycs and for Gapdh compared to that in the control group. Thus, Actn1 mRNA content in the flight group increased compared to the control. Meanwhile, the level of total DNA methylation in the groups B and V did not differ from the group G both in cardiomyocytes and in lung tissue cells. In the flight group F the level of total DNA methylation was higher than that in the control group G in cardiomyocytes and in the lung tissue cells. The content of mRNA of DNA methylases, cytosine demethylases Tet1, Tet3, histone acetylase and histone deacetylase did not change, but cytosine demethylase Tet2 mRNA content significantly decreased in cardiomyocytes, and in the lung tissue cells compared to the control group G, which could cause changes in total methylation level and transcription efficiency. The study was supported by program of the fundamental research SSC RF – IBMP RAS and program of RAS presidium “Molecular and cell biology”.