

SPACE LIFE SCIENCES SYMPOSIUM (A1)  
Human Physiology in Space (2)

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MICROARRAY ANALYSIS REVEALS CHANGES IN BLOOD AND SALIVA GENE EXPRESSION  
PROFILES IN RESPONSE TO ARTIFICIAL GRAVITY AS EXPERIENCED ON THE SHORT-ARM  
HUMAN CENTRIFUGE**Abstract**

Exercise countermeasures employed to date do not fully protect the cardiovascular and musculoskeletal systems during prolonged spaceflight. Ground-based research suggests that it is necessary to perform exercise countermeasures within some form of artificial gravity (AG) to prevent microgravity deconditioning. Short-arm human centrifuge is being investigated as an AG model to help to counteract the physiological deconditioning of long duration spaceflight. The molecular changes induced by AG has not been studied intensively. The aim of our work was to investigate gene expression patterns in blood and saliva of healthy volunteers undergoing a 30 min continuous and discontinuous AG protocol. The results are compared with the changes induced by a 30 min bout of aerobic exercise. Eight healthy volunteers were submitted to the three protocols. Blood and saliva samples were taken before and after the intervention. Gene expression analysis was analyzed using microarray technology. Preliminary results of 5 individuals indicate that 129 genes were differentially expressed as a results of the continuous protocol. The aerobic exercise intervention changed the expression of 806 genes (n=9). Fifty eight genes were in common between the 2 gene lists and their trend in expression was the same. Insulin growth factor 1 (IGF1) was upregulated in both conditions. For both interventions we identified a molecular network that could be associated with  $\text{NF}\kappa\beta$  activity. We also found that 34 genes that were differentially expressed in blood upon the continuous AG exposure showed the same significant expression trend in saliva. One hundred and thirty two genes in saliva were altered in expression after aerobic exercise. Our preliminary results indicate that genome-wide gene expression analysis can be used to study molecular changes during AG exposure. The data can help to shed light on the molecular systems and pathways that are influenced. We will complement our study with data from more test subjects. Moreover, we will study the difference between a continuous and discontinuous AG protocol at the gene expression level.