IAF MICROGRAVITY SCIENCES AND PROCESSES SYMPOSIUM (A2)
Science Results from Ground Based Research (4)

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OMIC ANALYSIS OF SIMULATED-MICROGRAVITY INDUCED TITAN CELLS BY A YEAST ISOLATED FROM THE INTERNATIONAL SPACE STATION

Abstract

The International Space Station (ISS) constitutes an extreme environment that experiences high radiation and microgravity stressors which impacts both its human crew and their microbial counter parts. Recently, the first novel Eukaryote was isolated from the ISS, this yeast named *Naganishia tulchinskyi* demonstrated the ability to form enlarged Titan cells when grown in simulated-microgravity environments. It is unclear if there are physiological and or molecular differences between these Titan cells and the standard gravity grown cells. Here we show that significant molecular alterations are occurring within the simulated-microgravity grown *N. tulchinskyi* when compared to standard gravity grown cells. Titan cells are substantially larger than standard cells (10um and 4um diameters, respectively); however, they grow slower than their controls producing fewer CFUs ($10^6 and 10^8 CFUs, respectively$). $Proteomic and transcriptomic analysis both indicate th$ $microgravity grown cells group into statistically distinct expression groups, as opposed to all of the standard gravity controls w$ $microgravity when grown in warmer conditions (30C, rather than 23C). Transmission electron microscopy tomography indic$ $microgravity and standard gravity grown cell controls. Our results demonstrate that simulated-microgravity alters N. tulchi$ $microgravity in combination with higher temperatures is crucial in the formation of Titan cells. Further research is needed to d$ $microgravity responsive lipids do end up aiding N. tulchinskyi survival in microgravity conditions aboard the ISS, they could be o$