Title - Impact of $KRAS^{G13D}$ Mutation on Colorectal Cancer Cell Line HCT116 Organelle Structure, Function, and Growth

Program of Study – Department of Biology

Presentation Type – Choose one of the following: Theoretical Proposal Poster

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Abstract: KRAS mutations are found in 20% of all cancers and 40% of colorectal cancers specifically in the G12 and G13 codons. Ras is a protein that is downstream of several G-protein coupled receptors in a pathway integral to the regulation of programmed cell death called apoptosis. Many cancer cells have a KRAS mutation that results in the deregulation of these apoptotic pathways, which allows uncontrolled cell proliferation and the formation of a tumor. One such method of this apoptosis is the release of calcium ions (Ca^{2+}) from the endoplasmic reticulum (ER) and mitochondria and their subsequent interaction with caspases. Currently, research has not studied the effects of the $KRAS^{G13D}$ mutation on the growth, structure, and function of the colorectal cancer cells organelles, particularly the ER and mitochondria. This research would establish the impact of the mutation on the normal calcium storage in the colorectal cancer cell line HCT116, as well as establishing how this allele mutation impacts the overall organelle functions. Additionally, fetal bovine serum (FBS) is commonly added to cell cultures as it is rich in nutrients and provides the cell cultures with many growth factors. Due to its association with rapid cell growth and high efficacy yields, FBS is commonly utilized by industry and academia in the culturing of cells, however, is not present for normal biological cell growth. The impact of not using FBS in cell culture has not

been widely explored, and thus the effect on cell growth rate and viability is not known. Since FBS is so expensive, this research project will perform all colorectal cancer cell trials in duplicate – one with FBS and one without – to determine whether cells can be cultured successfully without the FBS. These studies will be performed via cell culture counts as well as flow cytometry techniques with corresponding organelle stains.