CHARACTERIZATION OF THE DBC1-INDUCED CELL DEATH PATHWAY. Jordan Myers[1,2], *Kate Wright, PhD.[2,3] *jrm4989@rit.edu*, *lkwsbi@rit.edu* *The McNair Scholars Program (Academic Affairs)[1], Rochester Institute of Technology[2], University of Rochester Medical Center[3]*

The Deleted in Bladder Cancer Chromsome Region 1 (DBC1) tumor suppressor gene has been shown to induce non-classical apoptosis in cultured human bladder tumor cells. Cell lines that were transfected with an expression vector containing DBC1 fused to enhanced green fluorescent protein (EGFP) demonstrated a novel death phenotype where cells would round, detach, and appear apoptotic, but showed neither DNA fragmentation nor caspase-3 activity; two hallmarks of the classical apoptosis pathway. The purpose of this study was to determine if the 293T human embryonic kidney cell line would be a suitable model for DBC1-incuded cell death and to attempt to further classify the programmed cell death pathway. Using fluorescence microscopy, cell rounding and detachment were observed in 293T cells with the EGFP-DBC1 expression vector 24 hours post transfection. However, cells expressing only EGFP did not display this pattern, suggesting that DBC1 can induce the non-classical pathway in the 293T cell line. DNA extracted from these cells will be examined for a ladder pattern, typical of classical apoptosis, with agarose gel electrophoresis. To further investigate the pathway, activity of Cathepsin B, a lysosomal protease involved in some forms of apoptotic-like programmed cell death, was detected and analyzed. Preliminary results suggest that the protease is not involved in the pathway; localization in the cytoplasm was not found. Future work includes a deeper analysis of other possible mediators of the pathway.