

MASON WINKIE and BRUCE ANTHONY Ph.D., Dept of Chemistry and Biochemistry, West Virginia Wesleyan College, Buckhannon, WV, 26201. Bioinformatics review of alcohol exposed neuronal stem cells and transcription factor consensus sequences in cell cycle progression genes.

Previous studies from microarray analysis of neuronal stem cells exposed to moderate levels of alcohol, suggested that alterations in proliferation and induced apoptosis may well be associated with a distinct set of transcription factors and associated consensus sequences in key gene sets responsible for G1/S phase progression and DNA synthesis. The objective of the study was to gather existing information on the Fox1, E₂F₁, DP-1, DP-2, DP-3, AP-1, and SP-1 transcription factors and examine their interaction with the promoter regions of genes involved with cell cycle progression through a bioinformatics approach. To complete this review, data was compiled using the Unipro UGENE program. Using this program, the promoter regions of genes of interest were aligned with the known DNA consensus sequences targeted by the transcription factors. Based on the alignments – or lack thereof – conclusions were drawn as to which transcription factors exert most influence on controlling proper cell cycle progression. Data showed interactions among several of the transcription factors with the multiple regions in the promoter regions of almost all the examined genes. Based on the discovered consensus sequences and their influence on the expression rates of genes necessary for cell cycle progression, this study provides plausible evidence of transcription factors worth targeting for controlling specific genes in cell cycle progression.