

Poster III-6

Gene Expression Analysis of Malignant Gliomas

Sibenaller, Zita, A. , Ryken, Timothy C.

University of Iowa, Iowa City, IA, USA

Cancer is the result of cellular transformation brought about by a complex set of events involving three major steps: initiation (the accumulation of genetic alterations), promotion (uncontrolled growth) and progression (selective survival of transformed cells and their capacity to invade distant sites). Brain tumors are a leading cause of death among young children and adults with estimates that approximately 20,000 people in the United States will be diagnosed as having a malignant glioma this year. There are several approaches available for the treatment of malignant brain tumors, however no one approach is optimal due in part to the fact that the molecular mechanisms that occur during the development of these tumors are not well understood. It appears that glial tumors are heterogeneous and develop by different mechanisms involving different genetic pathways. These malignant tumors may develop *de novo*, through de-differentiation of mature glial cells or by the increasing acquisition of genetic abnormalities resulting in a malignancy. Often tumors that have an original diagnosis of being low grade will acquire increasing genetic alterations and progress to a more malignant state. Defining the molecular events that occur during tumor development will facilitate the development of specific molecular targets to combat this disease. Microarray technology allows analysis of thousands of genes simultaneously providing a transcription profile for each sample tested. Interpretation of the enormous amount of data generated is complex making it difficult to focus on the differences in gene expression that may ultimately represent the most significant changes between normal and pathological processes. In order to better understand at a molecular level the significant genetic changes that occur in high-grade malignant brain tumors, studies were done to establish primary cell cultures from excised specimens followed by microarray analysis. Initial evaluations using GeneSpring™ software for data analysis demonstrates changes of gene expression (both up-regulation and down-regulation) of at least 5-fold in approximately 300 genes when compared to the normal brain control. Further analyses using multiple computational tools is required to narrow the focus for further investigations in the search for specific molecular targets that will be useful in treating this deadly disease.