Discovering Biological Basis of Age-Related Survival Disparities in Brain Cancer: A Bioinformatics Approach

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Cudahy Hall, Room 401

Glioblastoma multiforme (GBM) is the most common primary brain tumor in the USA and European countries, with about 3 in 100,000 people newly diagnosed with GBM each year, accounting for > 51% of all gliomas. Age has been identified as an independent significant prognostic factor for survival. An analysis conducted by the Radiation Therapy Oncology Group showed that median survival of GBM patients aged 60 or older was 7.5 months compared to 16.2 months in patients younger than 40 years old. However, the biological basis for the difference in clinical outcome is mostly unknown. Discovering genes and pathways that would explain age-specific survival difference could generate opportunities for novel therapeutics for GBM.

To understand the biological basis of age-related survival disparities in GBM, we integrated high-throughput genomic, genetic, epigenetic and clinical datasets of a cohort of GBM patients in The Cancer Genome Atlas (TCGA) project to discover age-specific signatures at the transcriptional, genetic, and epigenetic levels. We validated our findings on an external data set. We found major age-specific signatures at all levels including the upregulation of angiogenesis-related genes in older GBMs. These age-specific differences in GBM may in part explain the preferential effects of anti-angiogenic agents in older GBM and pave the way to a better understanding of the unique biology and clinical behavior of older versus younger GBMs.

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For further information: see http://www.marquette.edu/mscs/resources-colloquium.shtml
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