Glioblastoma Pathophysiology

Glioblastoma is found to have many genetic and epigenetic mutations. The mutations are important to identify and classify in order to understand the tumor behavior and treatment resistance throughout the clinical course. Due to the presence of different triggering mutations in addition to key mutations in the GBM stem cells, glioblastoma is classified into primary tumors arising from neural stem cell precursors and secondary tumors arising from mutations in mature neural cells like astrocytes. Alteration in genetic information, causing expression and suppression of genes compared to their physiological levels in healthy brain cells, lead to both cellular and extracellular matrix changes resulting in a multiform number of biochemical forms [1].

A significant proportion of the human transcriptome, Long non-coding RNAs (lncRNAs) play pivotal roles in several aspects of glioblastoma (GBM) pathophysiology including proliferation, invasion, radiation, and temozolomide resistance, and immune modulation. The majority of lncRNAs exhibit tissue- and tumor-specific expression, lending them to be attractive targets for therapeutic translation. In recent years, unprecedented progress has been made toward our understanding of lncRNA in GBM. In this review, we discuss the function of lncRNAs, including specific lncRNAs that have critical roles in key aspects of GBM pathophysiology, and the potential clinical relevance of lncRNAs for patients with GBM [2]

1)
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2)
Villa GR, Chiocca EA. The Role of Long non-coding RNAs in Glioblastoma: What the Neurosurgeon Should Know. Neurosurgery. 2023 Mar 7. doi: 10.1227/neu.0000000000002449. Epub ahead of print. PMID: 36880757.