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What causes brain cancer? Understanding glioblastoma at the genetic, molecular level

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Glioblastoma is the most common and most lethal form of brain tumor in people. Research published in the *International Journal of Computational Biology and Drug Design* offers a novel way to determine what biological functions go awry when the tumor first begins to form. Understanding the problems at the molecular level might one day reveal the underlying mechanism of carcinogenesis in glioblastoma and ultimately lead to treatments or even preventative measures.

This form of brain tumor account for more than half of all cases in which the tumor is within the tissues of the brain and a fifth of cases in which a tumor is present within the skull.

Zhongming Zhao and colleagues at Vanderbilt University, in Tennessee, explain how problems that occur during the transcription of the genetic code for making proteins may play a role in the formation of a glioblastoma. These might arise through changes in the genetic materials itself or alterations to the molecules involved in regulating the transcription process. In their latest research, the team has tested the possibility that microRNAs (miRNAs) and transcription factors (TFs) might somehow regulate the genes glioblastoma. With this in mind, the researchers carried out a computer search of appropriate databases to uncover any links between these components of the genetic machinery and glioblastoma.

Although cancer exists in many different forms and is not a single disease but a complex array of different diseases, there are certain

characteristics that define the different forms: self-sufficiency in growth signals, insensitivity to antigrowth signals, evading programmed cell death, limitless replicative potential of cells, sustained blood-vessel growth, evasion of the immune system, tissue invasion and spreading through the body in metastasis. Insights into these processes at the molecular level is now possible thanks to the advent of vast databases of genomic and biochemical information related to different types of cancer.

The Vanderbilt team has now searched three databases miR2Disease, HMDD (human miRNA-associated disease database) and PhenomiR, to find regulatory networks specific to glioblastoma. To do so they integrated data on glioblastoma-related miRNAs, TFs and genes. They utilized a well-known target-prediction tool, TargetScan, to trawl the databases and identified 54 so-called feed-forward loops (FFLs), these are molecular control systems involved in transcription and the required signaling processes. Follow up work revealed these FFLs to have functions important to carcinogenesis as well as unique functions specific to each FFL.

"Our work provided data for future investigation of the mechanisms underlying glioblastoma and also potential regulatory subunits that might be useful for biomarker discovery and therapy targets for glioblastoma," the team concludes.

More information: "Gene regulation in glioblastoma: a combinatorial analysis of microRNAs and transcription factors" in Int. J. Computational Biology and Drug Design, 2011, 4, 111-126

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