Computational Screening of Secretory Proteins with Brain-Specific Expression in Glioblastoma Multiforme

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Abstract: Glioblastoma multiforme (GBM) is a widely spread and fatal primary brain tumor with an increased risk of relapse in spite of aggressive treatment. The current procedures for GBM diagnosis include invasive procedures i.e. resection or biopsy, to acquire tumor mass. Implementation of negligibly invasive tests as a potential diagnostic technique and biofluidbased monitoring of GBM stresses on discovering biomarkers in CSF and blood. Therefore, we performed a comprehensive in silico analysis to identify potential circulating biomarkers for GBM. Initially, six gene and protein databases were utilized to mine brain-specific proteins. The resulting proteins were filtered using a channel of five tools to predict the secretory proteins. Subsequently, the expression profile of the secreted proteins was verified in the brain and blood using two databases. Additional verification of the resulting proteins was done using Plasma Proteome Database (PPD) to confirm their presence in blood. The final set of proteins was searched in literature for their relationship with GBM, keeping a special emphasis on secretome proteome. 2145 proteins were firstly mined as brain-specific, out of which 69 proteins were identified as secretory in nature. Verification of expression profile in brain and blood eliminated 58 proteins from the 69 proteins, providing a final list of 11 proteins. Further verification of these 11 proteins further eliminated 2 proteins, giving a final set of nine secretory proteins i.e. OPCML, NPTX1, LGI1, CNTN2, LY6H, SLIT1, CREG2, GDF1 and SERPINI1. Out of these 9 proteins, 7 were found to be linked to GBM, whereas 2 proteins are not investigated in GBM so far. We propose that these secretory proteins can serve as potential circulating biomarker signatures of GBM and will facilitate the development of minimally invasive diagnostic methods and novel therapeutic interventions for GBM.

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