UNVEILING PROGNOSTIC HUB GENES FOR THE MANAGEMENT OF GLIOMAGENESIS THROUGH TRANSCRIPTOME PROFILING

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Despite recent advancements, glioma prognosis remains poor, with a median survival of 15 months with a high relapse rate. Thus, the current study aimed to shed light on identifying prospective candidate hub genes as potential biomarkers related to the pathogenesis of gliomas. The integrative pipeline, including quality control, normalization, principal component analysis (PCA), and immunohistochemistry, identified differentially expressed genes (DEGs), which were then validated. Gene ontology (GO) and KEGG pathway analysis were utilized to functionally elucidate the hub genes. Interestingly, the present study identified novel hub genes such as TP53, SRC, UBA52, UBB, and CDK1. Of note, ours is the first report on the UBA52 and UBB which unveils the use of these hub genes as potential biomarkers. These genes were mainly involved in crucial oncological pathways that annotated their resemblance with glioma. Finally, potential candidate drugs were predicted against three key gene targets, namely TP53, SRC and CDK1, using the DGIdb database to manage glioblastoma effectively. Indeed, we believe that the exploration of UBB and UBA52 would present exciting opportunities for scientific advancement in the field of glioma treatment strategy. Overall, the results from our study provide a new avenue for the precise understanding of prognostic and diagnostic biomarkers that could serve as specific therapeutic targets for averting gliomagenesis in the near future.

Key words: *glioma WHO grades, differential gene expression, hub genes, protein interaction networks, drug-gene interaction.*

ВИЯВЛЕННЯ ПРОГНОСТИЧНИХ ВУЗЛОВИХ (ХАБІВ) ГЕНІВ ДЛЯ КОНТРОЛЮ ГЛІОМАГЕНЕЗУ ЗА ДОПОМОГОЮ ТРАНСКРИПТОМНОГО ПРОФІЛЮВАННЯ

Попри нещодавні наукові досягнення, прогнозування гліоми залишається на низькому рівні, середній термін виживання становить 15 місяців, а частота рецидивів є високою. Тому метою даного дослідження було пролити світло на ідентифікацію потенційних вузлових генів (генів-хабів) як можливих біомаркерів, пов'язаних із патогенезом гліом. Інтегративний підхід, що охопив контроль якості, нормалізацію, аналіз головних компонентів (PCA) та імуногістохімію, дозволив ідентифікувати диференційно експресовані гени (DEG), які потім були валідовані. Для функціонального дослідження вузлових генів було використано генну онтологію (GO) та аналіз шляхів KEGG. Цікавим є той факт, що в цьому дослідженні було ідентифіковано нові вузлові гени, зокрема, TP53, SRC, UBA52, UBB та CDK1. Варто зазначити, що наше дослідження є першим звітом про UBA52 та UBB, який розкриває використання цих вузлових генів як потенційних біомаркерів. Ці гени були в основному залучені до важливих онкологічних шляхів, що підтверджувало їх схожість з гліомою. Зрештою, за допомогою бази даних DGIdb було передбачено потенційні лікарські препарати для ефективного лікування гліобластоми, спрямовані на три ключові генетичні мішені, а саме TP53, SRC та CDK1. Ми вважаємо, що дослідження UBB та UBA52 відкриє захоплюючі можливості для наукового прогресу в галузі стратегії лікування гліоми. Загалом, результати нашого дослідження відкривають нові перспективи для точного розуміння прогностичних та діагностичних біомаркерів, які можуть слугувати конкретними терапевтичними мішенями для запобігання гліомагенезу в найближчому майбутньому.

Ключові слова: ступені гліоми за ВООЗ, диференціальна експресія генів, вузлові гени, мережі взаємодії білків, взаємодія «препарат-ген».

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