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A bioinformatics approach to reveal common genes and molecular pathways shared by cutaneous melanoma and uveal melanoma

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Abstract

Background Melanomas are highly aggressive in nature known for metastasis and death. Melanocytes that gave rise to melanomas are neural crest progenitor cells. Our research was primarily concerned with uveal melanoma (UM) and cutaneous melanoma (CM), respectively. Although they both have the same melanocytic origin, the biology of their respective is different.

Aim The aim of our study was to recognize the common differentially expressed genes (DEGs) between UM and CM.

Methodology The gene expression profile was downloaded from the GEO and analyzed by GEO2R to recognize DEGs. By applying DAVID, GO, and KEGG, pathway enrichment analysis was performed. PPI of these DEGs was analyzed using STRING and visualized by Cytoscape and MCODE. Further, we utilized HPA and GEPIA to obtain Kaplan–Meier graph for survival analysis in order to assess the prognostic value of hub genes.

Results We examined the UM and CM datasets and discovered three common upregulated and eight downregulated DEGs based on computational analysis. HMGCS1 and ELOVL5 were shown to be enriched in a variety of altered molecular pathways and pathways in cancer. Overexpression of HMGCS1 and ELOVL5 was linked to a poor prognosis in CM.

Conclusion Computational evaluation found that HMGCS1 and ELOVL5 were upregulated in both melanomas. Enrichment analysis showed that these genes are involved in cancer metabolism pathway and associated with poor prognosis in CM. However, the molecular study of these genes in UM is limited. Therefore, a better understanding of the cancer metabolism pathways should be carried to pave the way for clinical benefits.

Keywords Uveal melanoma, Cutaneous melanoma, Metastasis, Bioinformatics

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