PROTEOMIC PROFILING OF THE CROSSTALK BETWEEN ENDOTHELIAL AND MELANOMA CELLS

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Melanoma is a highly aggressive skin cancer, known for its invasion capacity and metastatic potential. The tumor microenvironment (TME) includes not only transformed cells but also immune cells, pericytes, and stromal cells that contribute to cancer progression. Understanding the signaling interactions between cancer cells and stromal cells within the TME is crucial for comprehending cancer progression. Endothelial cells, which form blood vessels, play a key role in angiogenesis, an essential process for cancer growth. This study aimed to identify the proteome changes associated with the interaction between endothelial and melanoma cells using stable isotopic labeling of amino acids in cell culture (SILAC). Conditioned media (CM) from melanoma cell lines (A375, WM1366, and SH4) and endothelial cells (HUVEC-CS) were collected from a co-culture model and used in various functional experiments. Functional assays, including cell migration, angiogenesis, MTT, and clonogenic assays, were conducted to assess the effects of different CMs on melanoma and endothelial cells. Results showed significant effects from the co-culture CMs, such as increased colony formation, proliferation, and tube formation in endothelial cells induced by CM from the metastatic SH4 cell line. Moreover, CM from primary melanoma cells significantly enhanced endothelial cell migration. SILAC culture was utilized to study the crosstalk between tumor and endothelial cells. Proteomics analysis revealed differences in protein abundance related to angiogenesis, proliferation, and migration in the co-cultured cells and identified specific proteins for each cell line.

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