Downregulation of LAMB3 altered the carcinogenic properties of human papillomavirus 16 positive cervical cancer cells

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September 1, 2023

Abstract

Nearly all cervical cancer cases are infected with high risk (HR)-HPV types, with HR-HPV16 accounting for more than 50%. The mechanism of cervical cell transformation is related to the powerful action of viral E6 and E7 oncoproteins. Transcriptomic sequencing (RNA-seq) data from HPV16 positive and HPV negative cervical cancer cell lines were utilized to identify upregulated genes and their associated pathways. There were 593 overlapping upregulated genes (fold change >4) found in HPV16 positive cell lines. According to gene ontology analysis, these genes were predominantly expressed in extracellular region and plasma membrane that play a role in protein binding and cell adhesion molecule binding, leading to response to stimulus and tissue development. KEGG pathway analysis showed that the most significant pathways were metabolic pathways, pathway in cancer, MAPK signaling pathway, and PI3K-AKT signaling pathway. The laminin subunit beta-3 (LAMB3) gene was chosen for functional analysis. LAMB3 knockdown decreased cell migration, invasion, anchorage dependent- and anchorage independent-cell growth and increased number of apoptotic cells of HPV16 positive cervical cancer cells. These effects were linked to a decrease in protein levels involved in the PI3K-AKT signaling pathway and increased p53 protein. This study demonstrated that LAMB3 could promote cervical cancer cell migration, invasion and survival.

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