



SEXUALLY TRANSMITTED INFECTIONS, HIV/AIDS

TRANSCRIPTIONAL REGULATION OF GENES IN CERVICAL EPITHELIAL CELL LINE CONTAINING HPV16 E6

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Introduction: The life cycle of human papillomaviruses (HPVs) is strictly linked to the differentiation of their natural host cells. The HPV E6 oncoproteins can delay the normal differentiation program of cervical epithelial cells. However, the exact mechanisms responsible for this are not so much clear currently. E6 protein encoded by HPV early genes plays an important role in HPV infection.

Objective: The goal of this study was to investigate the effects of HPV16 E6 oncoproteins on the expression of genes in transfected H8 stable cell line. The differentially expressed genes may help us understand the infection of HPV16 more comprehensively and explore the specific role of E6 protein in this process.

Materials and Methods: The expression profile of cervical epithelial H8 stable cell line containing HPV16 E6 gene was analyzed by microarray. Quantitative real-time PCR (qRT-PCR) was performed to confirm the microarray data. HPV16 E6 was also knocked down in SiHa cells for further verification.

Results: A total of 2084 genes were identified to be expressed significantly differentially between HPV16 E6-H8 stable cell line and control cell line, among which 844 genes were up-regulated and 1240 genes were down-regulated with fold-changes N[?]2.0 between the two groups. The most significantly enhanced genes expression in HPV 16E6-H8 cells were OLFML3, LUM, MAPK4 and EDA2R, while TDRD9 expression was down regulated obviously. LUM was significantly decreased upon HPV16 E6 knockdown in SiHa cells.

Conclusions: The gene expression profile of HPV16 E6-H8 stable cell line may help us to better understand the role of E6 oncoprotein in the productive virus life cycle, and also in virus-induced carcinogenesis.





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