

Molecular profile of head and neck squamous cell carcinomas bearing p16 high phenotype.

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Source

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Abstract

BACKGROUND:

We sought to determine biomarker expression differences in head and neck squamous cell cancers (HNSCCs) based on p16/human papillomavirus (HPV) classification. In addition, our aim was to explore how expression of biomarkers is modulated after E6/E7 repression in HPV16⁺ oropharyngeal cancer cells.

METHODS:

HPV16⁺ and HPV⁻ HNSCC cells were infected with retroviruses expressing short hairpin RNA targeting HPV16 E6/E7. Components of the epidermal growth factor receptor (EGFR) pathway before and after E6/E7 gene silencing were analyzed by immunoblotting and qRT-PCR. Protein expression of 13 biomarkers was analyzed using AQUA on a tissue microarray (TMA). The HPV16 status was determined using HPV16 in situ hybridization (ISH).

RESULTS:

In HPV16⁺ cells, E6/E7 silencing was associated with PTEN upregulation and reduction of phosphorylated EGFR. Tumors were classified into four categories based on the HPV and p16 status. HPV⁺/p16⁺ tumors expressed significantly higher levels of E-cadherin (P = 0.003), PTEN (P = 0.004), lower levels of PI3Kp110 and β -catenin (P = 0.07). There was a significant difference in overall survival (OS, P = 0.016) among the four subsets. The median OS was 24.83 months for p16⁻/HPV⁻ patients, 11.63 for p16⁻/HPV⁺ patients and was not reached for p16⁺/HPV⁻ and p16⁺/HPV⁺ groups.

CONCLUSIONS:

Aberrant EGFR signaling contributes to malignant conversion of HPV16⁺ HNSCC cells. These results validate β -catenin as a distinct biomarker in HPV⁺/p16⁺ HNSCC. Wnt signaling inhibitors merit exploration in HPV⁺/p16⁺ HNSCC.