

Public Abstract

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Title:COMPREHENSIVE PROFILING OF MICRORNA IN HUMAN PAPILLOMAVIRUS-ASSOCIATED SQUAMOUS CELL CARCINOMA OF THE HEAD AND NECK

A major problem in the application of our understanding of cancer biology is that treatment remains ineffective for certain individuals and there are few validated ways to choose among different treatment modalities for any given patient. In this study, we address poorly understood biochemical and molecular alterations underlying the pathobiology of a type throat cancer caused by Human Papillomavirus (HPV)(oropharyngeal squamous cell carcinoma, OPSCC).

The aim of the current study was to profile microRNA expression patterns in HPV+OPSCC to provide a more detailed understanding of pathological molecular events and to identify biomarkers for early diagnosis, improved staging, and prognostic stratification. Our long term goal is to use this unique HPV+ microRNA panel to develop a rapid, low-cost diagnostic platform to screen for oncogenic HPV infection using salivary samples.

We used laser-capture microdissection to harvest tumor cells from 23 patient samples. PCR-based microRNA profiling was used, and a unique data analysis model was developed that controlled for smoking status and age. Next, we performed additional profiling and validation using next-generation-sequencing data from The Cancer Genome Atlas (TCGA) project--showing strong concordance between datasets. Further validation was carried out in cell lines and human tissue cohorts using microRNA-in-situ hybridization assays.

We identified a unique HPV-associated microRNA profile. These targets will be used to develop a chip-based ion exchange membrane that could detect these microRNA sequences in a matter of minutes using salivary samples; delivering a solution that leads to early detection and better results for patients.