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

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Abstract

This dissertation addresses a major problem in the application of our understanding of cancer biology: 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 (oropharygneal squamous cell carcinoma) caused by the Human Papillomavirus (HPV)**.** Although clinical trials assessing differing management strategies for HPV+ relative to HPV- diseases are underway, currently it is common for HPV+ patients to be treated in the same manner as HPV-. However HPV+ tumors of the oropharynx are associated with powerful risk and survival stratification because these patients have prolonged progression-free responses and often, with appropriate surgical management, chemotherapy and radiation, experience complete responses that appear durable. Thus, early identification and characterization of this patient cohort is necessary specifically to tailor the care of these individuals to the unique biology of their tumors.

The work that follows describes the identification and validation of an “oncogenic microRNA panel” that likely represents the host response to an oncogenic HPV infection. This molecular signature may have utility to differentiate oropharyngeal tumors with different prognoses and thus distinct management strategies and facilitate mechanistic elucidation of molecular factors that contribute to OPSCC pathobiology.