Identification of a Gene Expression Signature Associated With Recurrent Disease in Squamous Cell Carcinoma of the Head and Neck


Squamous cell carcinoma of the head and neck (HNSCC) is the most common form of head and neck cancer, with about 40,000 new cases a year and 7,400 deaths. Annually, $3.2 billion is spent to treat these cancers. HNSCC is associated with smoking, tobacco use, and male gender, and has higher rates in African-Americans. HNSCC has a very high rate of local recurrence after being successfully treated. While a great deal is known about the molecular biology of HNSCC, accurate and reliable biomarkers that predict patients at highest risk for local recurrence have not yet been identified.

In an effort to identify genes and gene combination that may serve as biomarkers of recurrence, we studied 41 squamous cell carcinoma tumors (25 primary and 16 locally recurrent) from various anatomical sites and 13 normal oral mucosal biopsy samples from healthy volunteers using genome-wide microarray. We identified 2,890 genes as being different between primary and recurrent tumors. The function of the differentially expressed genes included cellular proliferation, extracellular matrix production, cytokine/chemokine expression, and immune response. Of particular interest, we noted a number of genes known to be involved in tumor invasion and metastasis. When examining which genes were not expressed, the recurrent tumors had an absence of an immune response signature, suggesting that modulation of tumor-specific immune responses may play a role in HNSCC recurrence. With this data we identified a number of genes as potential markers of HNSCC recurrence and were able to suggest a mechanism by which cancer may recur.

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