



Category: Cancer Genomics

Integrated Genomic Analysis of Early Stage Tongue Tumors Revealed Recurrent Transcript Fusions

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Abstract

Introduction: Tongue cancer is the most predominant form of oral cancer in developed countries with varying incidence in developing countries. In India, tongue cancer accounts for 21% of head and neck squamous cell carcinoma (HNSCC) and known to display occult node metastasis during early stages of disease. The major etiological factors associated with tongue cancer includes tobacco related products, alcohol and human papilloma virus (HPV) infections.

Objective: Portrait of genomic aberrations underlying the genome of tobacco/nut chewing HPV-negative early stage tongue tumors.

Materials and Methods: Whole transcriptome sequencing of 17 HPV-negative early stage tongue squamous cell carcinoma (TSCC) tumors and 4 HNSCC cell lines. Validation of findings in an additional set of 44 paired HPV-negative early stage TSCC tumor samples.

Results: Using bioinformatics approaches, we present the first glance of a portrait of 242 tumor specific transcript fusions, followed by exhaustive validation of 12 candidate fusion transcripts across 44 paired HPV-negative early TSCC tumor samples and 4 HNSCC cell lines. Comparative analysis of our data with various fusion databases revealed 48 previously described transcript fusions in various cancer types. We have identified and validated novel somatic recurrent fusion transcripts in tumor samples. Here, we present a comprehensive landscape of transcript fusions underlying the genome of HPV-negative early stage tongue tumors.

Conclusions: Characterization of the recurrent transcript fusions described here could serve as attractive candidates to facilitate in diagnosis of HPV-negative early stage TSCC patients.

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