Cancer Prevention Research

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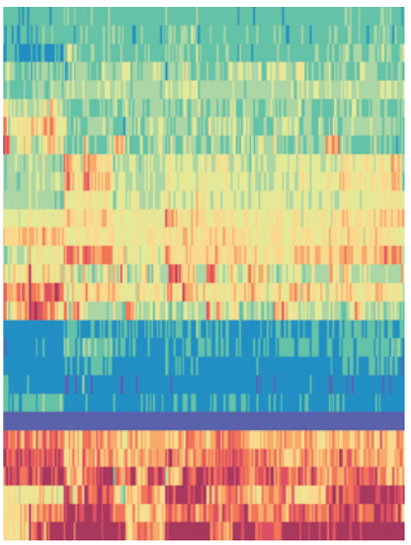

Oral squamous cell carcinoma (OSCC) is a highly debilitating and often fatal disease. Early detection is key, as early stage OSCC has a favorable prognosis and requires less aggressive treatment. Altered microRNA expression is a potential candidate for a molecular marker which can identify early malignant changes in the absence of clinically evident mucosal alterations. Yap et al (page 491) aimed to predict the presence of oral squamous cell carcinoma by selecting a panel of OSCC-related dysregulated microRNA identified jointly in data from formalin-fixed paraffin embedded (FFPE) and fresh frozen specimens for study in a novel sample type, oral swirls. Next generation sequencing (NGS) was used to determine microRNA fold changes in FFPE OSCC specimens relative to histologically normal epithelium (RDH-NGS). This data was placed with NGS of fresh frozen tissue data of The Cancer Genome Atlas database (TCGA). The cover shows a heatmap of expression values of TCGA-NGS data of the 29 microRNAs with fold changes greater (blue) or less (gray) than 1 (log2) in common with the RDH-NGS. Hierarchical clustering of samples was performed, with OSCC (n =292) displayed in black versus normal ($n = 30$) in red. Delineation of tumor and normal specimens utilizing these 29 candidate microRNAs yielded a sensitivity of 97.9% and specificity of 96.7%.

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