PRELIMINARY INSIGHTS INTO THE IMPACT OF TUMOR MICROBIOME IN HEAD AND NECK SQUAMOUS CELL CARCINOMA

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Background Head and neck squamous cell carcinoma (HNSCC) is a heterogeneous set of distinct malignancies. Recognized prognostic factors rely on clinical and biological features, consisting mainly of stage, site of disease, performance status, comorbidities, smoking history and human papilloma virus (HPV) status. However, patients clustered by these parameters still differ in their clinical behavior and therapy response. The impact of the tumor microbiome on human disease has been explored and discussed extensively. Evaluating the tumor microbiome is a promising new approach that could be used as a prognostic and predictive tool in HNSCC, with the potential for improved treatment options and better clinical outcomes.

Methods We utilized The Cancer Genome Atlas (TCGA) database to obtain RNA sequencing (RNAseq) data to identify microbes in HNSCC samples. We utilized ExoTIC, "Exogenous sequences in Tumors and Immune cells," a tool recently developed by Spakowicz et al. ExoTIC takes raw RNAseq reads and carefully aligns them to both human and non-human reference genomes to identify low-abundance microbes. We performed Cox proportional hazards regression to identify the microbes associated with overall survival (OS), controlling for age, stage, and smoking status.

Results We evaluated 498 RNAseq samples from TCGA (table 1). ExoTIC identified 5838 microbes including bacteria, viruses and fungi, of which 330 were statistically associated with OS. Interestingly, 20% (n=100) of samples had HPV virus which was significantly associated with improved OS (HR 0.59, CI 0.4–0.9, p<0.01). There were also several other viruses and bacteria associated with significantly improved OS.

microbial profile of HNSCC subtypes with clinical outcomes retrospectively and prospectively.

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Abstract 837 Table 1 Patient characteristics of TCGA dataset

Overall	
n	498
Age (mean (SD))	61.08 (11.92)
Sex = male (%)	366 (73.3)
Cancer Stage (%)	
Stage I	19 (3.9)
Stage II	94 (19.4)
Stage III	102 (21)
Stage IV	270 (55.7)
Primary Site (%)	
Oral cavity	108 (21.6)
Oropharynx	74 (15)
Hypopharynx	9 (1.8)
Larynx	111 (22.2)
Other	196 (39.3)
Vital Status = Deceased (%)	218 (43.7)

Conclusions We found the presence of certain microbes in tumor biopsies statistically correlated with OS in HNSCC patients. This supports further study into the presence and correlation of specific microbes with tumor subsite and outcomes. Assessing individual characteristics of a HNSCC subtype with its particular microenvironment (e.g., microbes) can lead to personalized treatment insights and improved outcomes. Our future research will validate and correlate the