Baseline CT Radiomic and Genomic Assessment of Head and Neck Squamous Cell Carcinoma

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Background

•Head and neck squamous cell carcinoma (HNSCC) is the 6th most common cancer globally, with **600,000 cases annually**. Mortality remains high despite advances in surgical, radiation, and pharmacological treatments.

•Precision treatments like targeted therapies and immunotherapies have shown promise in reducing HNSCC mortality. These methods rely on patients' genetic information to identify best candidates and monitor response.

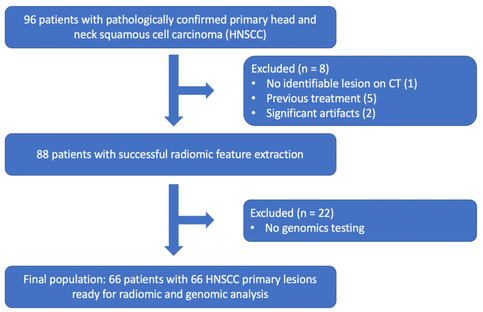
•Biopsy is the gold standard for obtaining genetic information but drawbacks include **cost, invasiveness, time, and sampling error.**

•Radiogenomics aims to correlate quantitative imaging features ("radiomics") with genomic information to create a "signature" so that genetic information for **all tumors** may be obtained quickly, non-invasively, and inexpensively to inform treatment management.

Specific Aims

The goal of this retrospective study is to determine the relationship between CT radiomic features and gene expression levels for six targetable genes (FGFR1, EGFR, FGFR2, FGFR3, EPHA2, PIK3CA) in order to optimize the management of patients with head and neck squamous cell carcinoma (HNSCC).

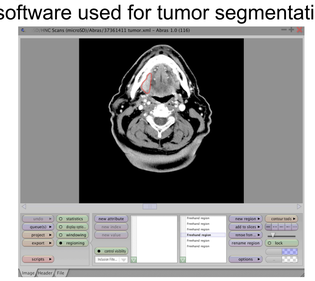
Patient Selection



Methods

- **66** patients with HNSCC primary lesions on contrast-enhanced CT.
- Primary lesion segmentation performed by researcher under supervision of fellowship-trained neuroradiologist. Single axial slice with the largest tumor volume was used for feature extraction.
- 142 radiomic features (22 first-order, 14 gray level co-occurrence matrix [GLCM], 5 Fractal, 17 Fourier, and 84 Laws' filter) calculated using in-house Matlab-based software.
- Gene expression profiling performed using Agilent 4 × 44 Kv2 expression arrays.
- Pearson correlation coefficients calculated using R. Raw *P* values adjusted using the false discovery rate (FDR) approach.

Figure 1: Screenshot of Abras software used for tumor segmentation.



Results

Patient demographics and tumor characteristics

Parameter	Classification	Value
Age (yr)	Mean ± SD (range)	56.8 ± 8.5 (41.5 – 81.2)
Gender	Male / Female	55 (83.3%) / 11 (16.7%)
Primary Site	Oropharynx / Hypopharynx / Larynx / Oral Cavity	36 (54.5%) / 6 (9.1%) / 10 (15.2%) / 14 (21.2%)
Alcohol Use	Never / Light / Heavy	6 (9.1%) / 34 (51.5%) / 26 (39.4%)
Tobacco Use	Never / Light / Heavy / Unknown	9 (13.6%) / 18 (27.3%) / 37 (56.1%) / 2 (3.0%)
Stage Group	I / II / III / IV (unknown) / IVA / IVB / IVC	2 (3.0%) / 0 (0.0%) / 2 (3.0%) / 1 (1.5%) / 49 (74.2%) / 11 (16.7%) / 1 (1.5%)

Radiogenomic correlations with FDR-adjusted *P* values < 0.05

Gene	Feature	Class	*r*	Raw *P*	FDR-adjusted *P*
FGFR1	Inertia	GLCM	0.367	0.002	0.006 ***
	Absolute value	GLCM	0.313	0.011	0.024 ***
	Contrast	GLCM	0.367	0.002	0.006 ***
	Difference Average	GLCM	0.313	0.011	0.024 ***
	Difference Variance	GLCM	0.371	0.002	0.005 ***
FGFR2	Box-Coarse	Fractal	0.326	0.008	0.018 ***
EPHA2	Entropy	GLCM	-0.278	0.024	0.049 ***

Figures

Figure 2: Heatmap of correlations between CT radiomic features and gene expression levels. Unsupervised hierarchical clustering was performed. All calculated correlations were used to generate this heatmap. *P* values were not considered. Gene names are located along the bottom. Radiomic feature names are located on the right side.

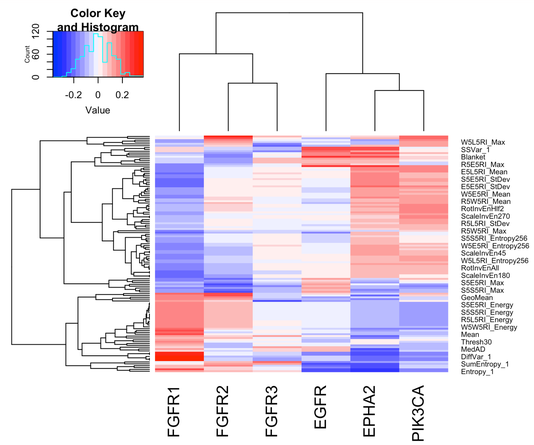


Figure 3a: Example of a primary tumor with high FGFR1 expression.

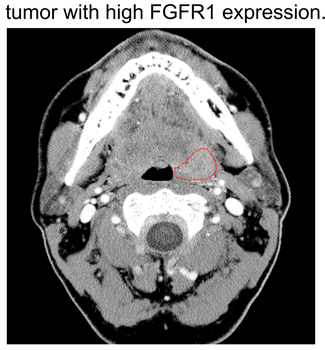
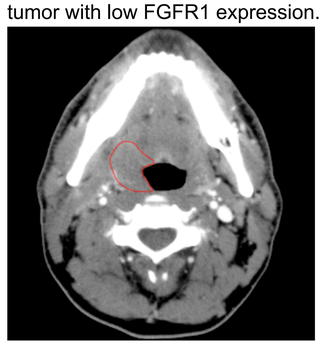


Figure 3b: Example of a primary tumor with low FGFR1 expression.



Conclusion

5 correlations between FGFR1 expression and GLCM features

CT GLCM features show promise for assessing FGFR1 expression.

Next steps: Create a model using the 5 GLCM features and assess ability to predict FGFR1 status.

Limitations

- Single institution retrospective study.
- No information regarding HPV status.
- Single axial CT slice per tumor.
- Tumor samples for genetic testing obtained via biopsy.

References

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