Quantitative Textural Analysis (QTA) in CT imaging: identifying markers for genetic instability and overall survival in cohort of previously treated metastatic pancreatic cancer (mPC)

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INTRODUCTION

Metastatic pancreatic cancer (mPC) is a rapidly fatal disease with limited treatment options that often carries bleak prognosis. Developing non-invasive tools to identify pancreatic tumor characteristics would aid in optimizing available treatments. Tumors with high numbers of dsDNA breaks identified as intrachromosomal copy number aberrations via CGH are often more susceptible to DNA-damaging chemotherapeutics. Identifying these tumors using standard-of-care CT imaging would allow targeted treatment to begin sooner.

AIMS

Quantitative textural analysis (QTA) is used to describe indiscernible CT imaging features that correspond to tumor microenvironment, vascularity, and local heterogeneity [Figure 1]. Relatable CT QTA parameters indicative of treatment options and prognosis have been developed for HCC, GBM, NSCLC, and colorectal cancer. The aim of this exploratory study was to identify QTA features that correlated with dsDNA breaks. We also sought to explore the prognostic value of QTA features in tumors and normal pancreatic tissue.

Quantitative Textural Analysis

TexRAD is a proprietary software-based QTA platform that measures pixel signal from multiple imaging modalities obtained during standard of care scans such as MRI, CT, and PET. Results are then displayed using a Histogram Frequency Curve (HFC). Imaging of a tumor region with low kurtosis and high dsDNA breaks (top image left, red curve) versus high kurtosis and low dsDNA breaks (bottom image left, green curve). Histogram frequency curve to right generated based on post-filtered pixels in tumor region.

METHODS

Metastatic mPC sites were biopsied and molecularly profiled. 85% of the cohort had 1-3 previous treatment regimens, and the remaining 15% had 4-6. Intrachromosomal copy number were assessed by CGH in tumor specimens. Patients were treated with commercially available cytotoxic regimens based on these individual molecular profiling results. Patients with available pre-biopsy abdominal portal-venous phase CT scans were obtained for retrospective analysis. There were 9 males and 6 females with a stage IV cancer from 34 – 71 years old (median 59) [Figure 5]. Analysis of pre-biopsy pancreas imaging was performed by drawing regions of interest around the primary pancreas adenocarcinoma (n=15) and the normal pancreas tissue when available (n=12). QTA parameters were derived using the TexRAD platform at texture filtering densities of medium (ssf=3) and coarse (ssf=5). These values were compared to intrachromosomal copy number aberrations per tumor and overall survival post-treatment using a Spearman’s rank correlation coefficient.

RESULTS: dsDNA BREAKS

Quantity of dsDNA breaks in tumor tissue correlated with more negative kurtosis values of the primary tumor mass using medium texture filtering (p = 0.034, n = 15, ssf=3) [Figure 3].

CONCLUSION

This exploratory study with admittedly limited sample size raises interesting possibilities about the use of QTA parameters as diagnostic tools and/or biopsy adjuncts in assessing pancreatic adenocarcinoma susceptibility to commercially available cytotoxic chemotherapeutics. Secondarily, entropy, a potential marker of heterogeneity and inflammation in the normal pancreas, represents an intriguing possibility for gauging prognosis in mPC.

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