

Radiomics features measured with multiparametric MRI predict prostate cancer aggressiveness.

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Background

Prostate cancer (PCa) diagnosis is generally based on transrectal ultrasound-guided biopsy. However, biopsies are invasive and prone to sampling error and carry a risk of infection. Therefore there is a significant need for more accurate and noninvasive techniques for determination of PCa aggressiveness. Radiomics analysis enables extraction of a large quantity of parameters that can be correlated to underlying tumor biology in several cancers, including PCa. The objectives of our study were to (1) assess the association of 1st and 2nd order radiomics features based on multiparametric magnetic resonance imaging (mpMRI) with histopathologic Gleason score, gene signatures and gene expression levels in PCa and (2) build machine learning models based on radiomics features to predict adverse histopathologic score and the Decipher genomics metastasis risk score.

Methods

A retrospective analysis of 64 PCa patients (mean age 64 y, range 41-76 y) that underwent radical prostatectomy in a single institution between 01/2016 and 01/2017 was performed. Inclusion criteria were mpMRI within 6 months before prostatectomy and no prior treatment. 226 mpMRI features (histogram and texture features, in addition to lesion size and PI-RADS score) were extracted from T2-weighted and diffusion-weighted imaging (DWI) data. mpMRI features were correlated with Gleason score, 40 gene expression signatures including Decipher and 698 PCa-related gene expression levels. Lasso-regularized logistic regression mpMRI machine learning models were built and evaluated for prediction of Gleason score ≥ 8 and Decipher score ≥ 0.6 .

Results

Fourteen mpMRI features significantly correlated with Gleason score (highest correlation $r=0.39$, $P=0.001$). Thirty-one texture and histogram features showed significant correlations with 19 gene signatures, particularly with PORTOS signature (strongest correlation $r=-0.481$, $P=0.002$). 40 DWI features correlated significantly with a total of 132 gene expression levels. Machine learning prediction models showed fair performance for prediction of Gleason score ≥ 8 ($AUC=0.72$) and excellent performance for prediction of Decipher score ≥ 0.6 ($AUC=0.84$).

Conclusions

Radiomics features based on mpMRI are promising markers of PCa aggressiveness on the histopathologic and genomics levels.

Conflict of Interest

Elai Davicioni is employed by GenomeDx Biosciences Inc.

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