



CT texture analysis in the differentiation of major renal cell carcinoma subtypes and correlation with Fuhrman grade

Yu Deng^{1,2} · Erik Soule³ · Aster Samuel² · Sakhi Shah² · Enming Cui^{2,4} · Michael Asare-Sawiri^{2,5} · Chandru Sundaram⁶ · Chandana Lall³ · Kumaresan Sandrasegaran^{2,7}

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Abstract

Objective CT texture analysis (CTTA) using filtration-histogram-based parameters has been associated with tumor biologic correlates such as glucose metabolism, hypoxia, and tumor angiogenesis. We investigated the utility of these parameters for differentiation of clear cell from papillary renal cancers and prediction of Fuhrman grade.

Methods A retrospective study was performed by applying CTTA to pretreatment contrast-enhanced CT scans in 290 patients with 298 histopathologically confirmed renal cell cancers of clear cell and papillary types. The largest cross section of the tumor on portal venous phase axial CT was chosen to draw a region of interest. CTTA comprised of an initial filtration step to extract features of different sizes (fine, medium, coarse spatial scales) followed by texture quantification using histogram analysis.

Results A significant increase in entropy with fine and medium spatial filters was demonstrated in clear cell RCC ($p = 0.047$ and 0.033 , respectively). Area under the ROC curve of entropy at fine and medium spatial filters was 0.804 and 0.841, respectively. An increased entropy value at coarse filter correlated with high Fuhrman grade tumors ($p = 0.01$). The other texture parameters were not found to be useful.

Conclusion Entropy, which is a quantitative measure of heterogeneity, is increased in clear cell renal cancers. High entropy is also associated with high-grade renal cancers. This parameter may be considered as a supplementary marker when determining aggressiveness of therapy.

Key points

- CT texture analysis is easy to perform on contrast-enhanced CT.
- CT texture analysis may help to separate different types of renal cancers.
- CT texture analysis may enhance individualized treatment of renal cancers.

Keywords Cone-beam computerized tomography · Image interpretation, computer-assisted · Clear cell renal cell carcinoma · Papillary renal cell carcinoma · Neoplasm grading

Abbreviations

ccRCC	Clear cell renal cell carcinoma	pRCC	Papillary renal cell carcinoma
CTTA	Computerized tomography (CT) texture analysis	RCC	Renal cell carcinoma
		ROC curve	Receiver operating characteristic curve
		SSF	Spatial scaling factor associated with CTTA

✉ Kumaresan Sandrasegaran
Sandrasegaran.kumaresan@mayo.edu

¹ Department of Radiology, The First Affiliated Hospital of Guangzhou Medical University, Guangzhou, China

² Department of Radiology, Indiana University School of Medicine, Indianapolis, IN, USA

³ Department of Radiology, University of Florida College of Medicine, Jacksonville, FL, USA

⁴ Department of Radiology, Jiangmen Central Hospital, Affiliated Jiangmen Hospital of Sun YAT-SEN University, Jiangmen, China

⁵ Department of Oncology, Hope Regional Cancer Center, Panama, FL, USA

⁶ Department of Urology, Indiana University School of Medicine, Indianapolis, IN, USA

⁷ Department of Radiology, Mayo Clinic, 5777 E. Mayo Blvd, Phoenix, AZ 85054, USA

Introduction

Renal cell carcinoma (RCC) is among the ten most common cancers with an annual incidence of 295,000 and mortality of 134,000 worldwide [1, 2]. RCC encompasses a heterogeneous group of malignant entities with distinct pathology, biology, and treatment considerations [3]. The three most common subtypes are clear cell RCC (ccRCC, approximately 75%), papillary RCC (pRCC, 15%), and chromophobe RCC (5%) [4]. The Fuhrman system is widely used for grading RCC and has prognostic value, independent from tumor subtype. RCC is categorized as Fuhrman grade 1–4 based on nuclear characteristics (i.e., size, shape, and contents) [5]. An increasing interest has been drawn to the accurate imaging characterization of RCC given different prognostic and management considerations for each subtype and Fuhrman grade [6–11]. Although the degree of contrast enhancement may be valuable for differentiation, there is considerable overlap of imaging features between subtypes, including tumor size, attenuation/signal intensity, and growth pattern [12].

CT texture analysis (CTTA) has emerged as a promising technique for assessing tumor heterogeneity and as a biomarker in predicting treatment response and prognosis [13–15]. A few studies have looked at the value of CTTA in differentiating benign and malignant renal tumors [16, 17]. Two prior studies investigated the differentiation of clear cell and papillary renal cancers using CTTA [18, 19]. A small study ($n = 53$) showed that machine learning-based CTTA was able to predict Fuhrman grade of renal cancers [20]. However, to our knowledge, no study has evaluated CTTA for its ability to both differentiate ccRCC from pRCC and predict the pathological grade of these tumors. The purpose of this study is to investigate CTTA parameters in the differentiation ccRCC from pRCC and to attempt prediction of the Fuhrman grade of RCC, based on a large cohort.

Materials and methods

Patients

This HIPAA-compliant retrospective study was approved by the Institutional Review Board with a waiver of informed consent. The pathology database was queried to find all the cases with histopathologic confirmation of ccRCC or pRCC between January 2007 and December 2014. Only cases with available contrast-enhanced CT studies before treatment were included. The inclusion and exclusion criteria were selected to minimize confounding variables (Fig. 1).

CT examination

All contrast-enhanced CT scans were performed on multi-slice CT systems (Philips Medical Systems), using similar protocols: 120 kVp, 180–450 mA with automatic tube current modulation, matrix of 512, field of view of 380–500 mm, and 4- or 5-mm reconstructed section thickness. Intravenous injection of 120 mL of 370 mg of iodine/mL of iopamidol (Isovue 370, Bracco Diagnostics) was delivered at 3 mL/s. The portal venous phase was obtained 75 s after commencement of contrast agent administration.

CT texture analysis

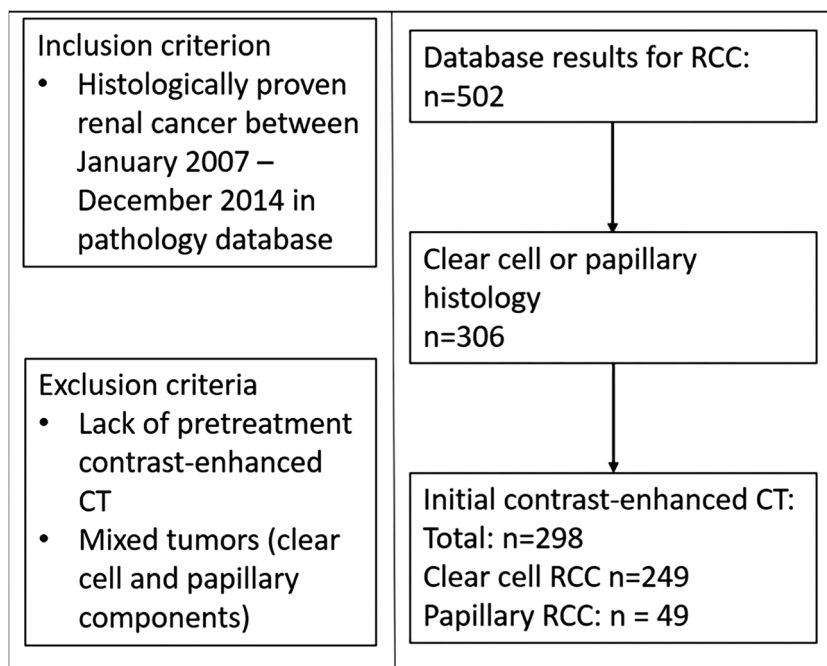
CT images were reviewed, and the maximum tumor diameter was recorded at a picture archiving and communications system (PACS) workstation (Synapse, Fujifilm Medical Systems) by a radiologist with 15 years of experience in body imaging (YD), blinded to pathology. The axial-enhanced CT image of the largest tumor cross section was identified, anonymized, and exported to a Digital Imaging and Communications in Medicine (DICOM) file. The DICOM files were uploaded to a cloud server with the TexRAD CTTA software (version 3.9, TexRAD Ltd.). A region of interest (ROI) was drawn to include the entire tumor (Fig. 2). The solid lesion algorithm was implemented which included only pixels above -50 HU within the ROI using “threshold” as padding (erosion scale = 0) for reducing edge artifact.

CTTA methodology using the filtration-histogram technique has been described elsewhere [13, 21–23]. Once ROIs are obtained, the CTTA software modifies the pixel data using several Laplacian spatial scaling factors (SSF), which extracts and enhances features of different sizes (mm) ranging from fine (SSF = 2 mm), medium (SSF = 4 mm), and coarse (SSF = 6 mm) texture scales. A fine filter tends to enhance tissue parenchymal features, while medium to coarse filters enhance vascular features [24]. The filtration step derives filtered maps, which are quantified to yield four parameters by histogram and statistical analysis. These parameters were mean value of positive pixels (average brightness considering only the positive pixel values), entropy (heterogeneity of pixel intensities), kurtosis (peakedness or sharpness of the pixel distribution), and skewness (asymmetry of pixel distribution). The mathematical process of calculating these parameters has been previously described [15, 25, 26].

Reference standard

The prospective histopathological reports were used as the reference standard. These were read by fellowship-trained histopathologists specialized in renal diseases. The Fuhrman grading was performed as per well-established guidelines [27]. As per multiple prior imaging and clinical studies

Fig. 1 Inclusion and exclusion criteria for study cohort



assessing outcome of renal cancers, we separated high-grade (Fuhrman 3, 4) from low-grade (Fuhrman 1, 2) cancers [20, 28–30].

Statistical analysis

The age of the patient and the size of the ccRCC and pRCC tumors were compared using two independent samples *t* test. The gender and Fuhrman grade between ccRCC and pRCC were compared using the chi-square test. A binary logistic regression analysis was performed to quantify any correlation between the CTTA parameters and the tumor size or histology. Receiver operating characteristic (ROC) analyses were used to assess the performance of CTTA parameters in the differentiation of subtypes of RCC. A multinomial logistic regression analysis was performed to correlate the CTTA parameters with Fuhrman grade. Statistical analysis was performed by using IBM SPSS Statistics for Windows, version 24.0 (IBM Corp.). Holm-Bonferroni correction of *p* values for multiple testing bias [31] was performed. A corrected *p* < 0.05 was deemed statistically significant.

Results

Demographics

The final cohort consisted of 244 patients with 249 ccRCC lesions (5 patients had two lesions) and 46 patients with 49 pRCC lesions (3 patients had two lesions). Epidemiological and clinical differences between the two groups of patients are

given in Table 1. The only significant difference noted was that pRCC patients were more likely to be males than ccRCC patients (*p* = 0.01).

Comparison of CTTA parameters between ccRCC and pRCC

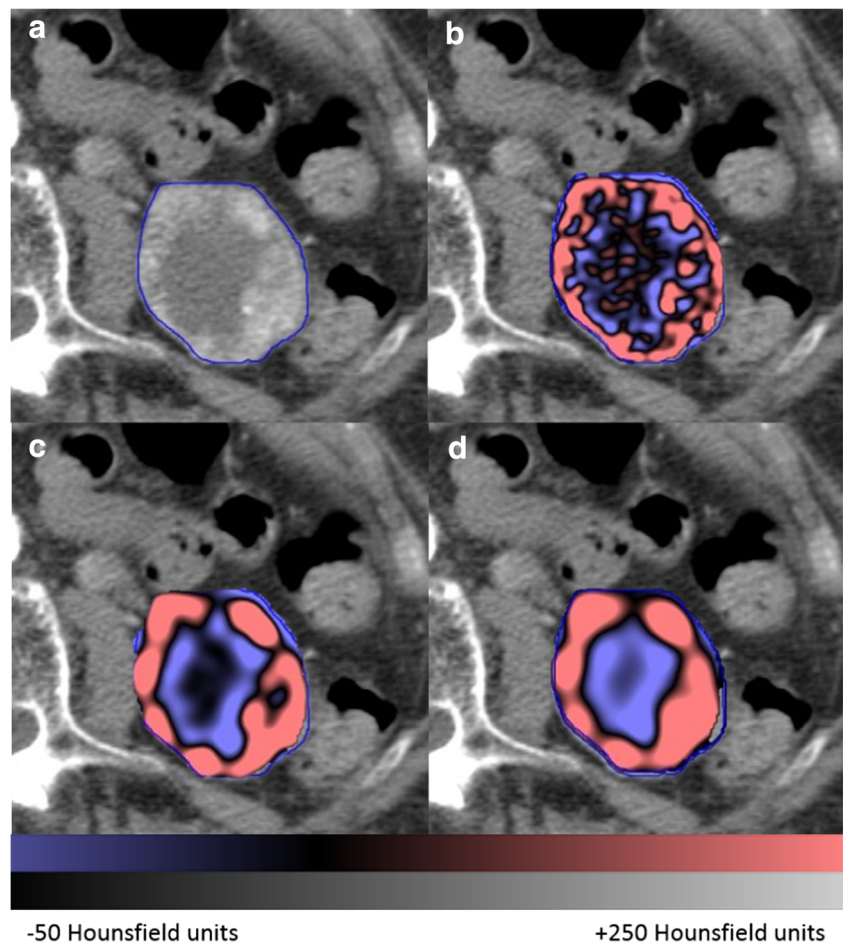
There was no significant difference in tumor sizes between the ccRCC and pRCC groups (*p* = 0.94). The CTTA parameters for ccRCC and pRCC and their value in differentiating the two entities are given in Table 2. The box and whisker plot of entropy values of renal cancers at medium spatial filter is given in Fig. 3. Entropy with fine and medium spatial filters of ccRCC was significantly higher than that of pRCC (*p* = 0.047 and 0.033, respectively).

Area under the ROC curves (AUC) of entropy at fine, medium, and coarse spatial filters were 0.804 with a 95% confidence interval of 0.755–0.848, 0.841 (0.803–0.888), and 0.822 (0.774–0.864), respectively (Fig. 4). Entropy greater than 5.34 at medium spatial filter had sensitivity and specificity of 77.5% and 83.7%, respectively, for diagnosing ccRCC.

Correlation between CTTA parameters and Fuhrman grade

High Fuhrman grade (3 and 4) cancers were associated with larger tumor diameter (*p* < 0.001) and a high entropy value (*p* = 0.01) with a coarse filter (SSF6). The other parameters were not significantly associated with high Fuhrman grade.

Fig. 2 CT texture analysis of ccRCC. **a** Delineation of tumor (blue line). **b–d** Color texture overlays of tumor outlined by ROI at fine (**b**), medium (**c**), and coarse (**d**) spatial filters. These images undergo pixel-by-pixel histogram analysis to yield CTTA parameters. When a fine spatial filter is applied, the internal structure of the tumor can be clearly seen



Discussion

CTTA has demonstrated promising diagnostic and prognostic capabilities for evaluation of malignancies and other disease processes, especially in the pulmonary, gastrointestinal, and genitourinary systems [32–34]. Further refinement and standardization of protocols and parameters may allow CTTA to be implemented in clinical practice. For example, in heterogeneous tumors such as RCC, a percutaneous biopsy of one region of the tumor may underestimate the overall tumor grade. Performing CTTA in this circumstance could function as a “failsafe,” triggering additional investigation and mitigating sampling bias. CTTA could also potentially spare biopsy or resection for poor surgical candidates. If the lesion appears unlikely to cause short-term morbidity and mortality, a multidisciplinary “wait and watch” approach may be selected.

The current paradigm of RCC imaging interpretation is based on a visual process which includes assessment of the shape, margin, as well as degree and heterogeneity of enhancement. These subjective methods do not adequately address discrepancies in the cellularity, angiogenesis, matrix, and areas of necrosis between different tumor subtypes (i.e., inter-tumoral heterogeneity) [35]. Texture analysis is an image

processing technique that can extract texture information in a quantitative manner, allowing for mathematical detection of changes in pixel intensity which may be visually imperceptible. This study explores the usefulness of texture analysis for the differentiation of ccRCC from pRCC and for predicting Fuhrman grade.

Prior studies have shown that ccRCC enhance substantially more than pRCC, particularly in the corticomedullary phase of enhancement [9, 10, 36–39]. Sensitivity and specificity of contrast-enhanced CT in distinguishing ccRCC and pRCC have been reported to vary from 70 to 98 and 62–92, respectively [9, 10, 12, 39]. Some studies have suggested that on the whole ccRCC are subjectively more heterogeneous than pRCC [40]. However, when heterogeneity was assigned a three-point score, there was substantial overlap in the scores of ccRCC and pRCC [41]. In another study, 84% of ccRCC and 74% of pRCC subjectively showed heterogeneous enhancement [12]. Thus, an objective score of heterogeneity, such as entropy seen in CTTA, may help increase specificity in some cases to distinguish ccRCC from pRCC. In such cases, CTTA may obviate need for additional imaging tests, such as MRI.

Among CTTA parameters, entropy was seen to be the best predictor for differentiation of ccRCC from pRCC. Entropy

Table 1 Patient characteristics

	Clear cell RCC (<i>n</i> = 249)	Papillary RCC (<i>n</i> = 49)	<i>p</i>
Age	60.1 (18–93 years)	62.7 (34–75 years)	0.18
Gender	M:F = 147:102	M:F = 38:11	0.01
Fuhrman grade (low/high)	173/76	30/19	0.26
AJCC stage (1/2/3/4)	187/15/40/4*	41/5/3/0	0.12
Tumor size in cm: mean (SD)	4.0 (2.6)	4.1 (2.7)	0.94

Except where indicated, data are numbers of patients

AJCC, American Joint Committee on Cancer staging classification: 7th edition

*No staging available in 3 patients

represents the randomness or irregularity of gray-value distribution, and heterogeneous tumors tend to have greater entropy [42]. In accordance with previous studies, ccRCC demonstrates higher entropy compared to pRCC, signifying increased intra-tumoral heterogeneity [41]. Entropy greater than 5.34 at medium spatial filter (SSF4) has sensitivity and specificity of 74% and 88%, respectively, to distinguish of ccRCC from pRCC, a significant improvement in specificity when compared to standard techniques. Chen et al also demonstrated increased entropy of ccRCC compared to pRCC (increased standard deviation and interquartile range), most apparent in the arterial phase of the CT examination [19]. Lubner et al found that entropy higher than 4.86 was the best predictor of ccRCC [18]. In addition, they found that high mean of positive pixels was associated with ccRCC. We did not find this to be the case. There are a few potential reasons for the differences between our paper and that of Lubner et al. Our cohort is much larger. The Holms correction for multiple testing bias that we used is thought to be more stringent than the Bonferroni correction [31] used in the paper of Lubner et al.

The heterogeneity of RCC as elucidated by CTTA also demonstrates a statistically significant association with Fuhrman grade in this study. High entropy at coarse filter correlates with high Fuhrman grade ($p = 0.05$). Various CTTA parameters have demonstrated efficacy for grading malignancy in multiple organs, highlighting the need for future research in this field. In a study of 44 patients with gliomas, the coarse texture entropy and uniformity are found useful in distinguishing between low- and high-grade tumors [43]. In addition to higher entropy, higher standard deviation, higher kurtosis, and positive skewness are postulated to represent increased intra-tumoral heterogeneity and portend poorer prognosis [44, 45]. Recent studies correlate imaging features to Fuhrman grade and find that intra-tumoral necrosis was a strong predictor of aggressive histology [46, 47]. Visually imperceptible intra-tumoral necrosis, however, may result in underestimation of tumor heterogeneity and aggressiveness. In a study of differentiation between lipid-poor angiomyolipoma and RCC based on unenhanced CTTA, Hodgdon et al find that visual analysis was less accurate than textural analysis [48]. In

Table 2 CTTA parameters in differentiating ccRCC from pRCC

Spatial filter	CTTA parameter	ccRCC*	pRCC*	<i>p</i> value**
Fine (SSF 2)	Entropy	8.3 (14.8)	− 4.9 (21.4)	0.047
	Mean pos.***	5.6 (0.3)	5.22 (0.35)	0.907
	Skewness	0.01 (0.48)	− 0.07 (0.51)	0.113
	Kurtosis	0.96 (4.27)	1.17 (2.34)	0.114
Medium (SSF 4)	Entropy	14.3 (28.1)	− 10.1 (29.0)	0.033
	Mean pos.***	5.6 (0.33)	5.1 (0.3)	0.076
	Skewness	− 0.01 (0.43)	0.15 (0.61)	0.524
	Kurtosis	0.18 (1.23)	1.90 (4.64)	0.085
Coarse (SSF 6)	Entropy	17.8 (37.9)	− 13.3 (30.1)	0.053
	Mean pos.***	5.54 (0.36)	5.1 (0.38)	0.055
	Skewness	− 0.09 (0.46)	0.18 (0.72)	0.634
	Kurtosis	− 0.05 (0.86)	1.63 (3.76)	0.260

*Mean (standard deviation) of CTTA parameter values

***p* values after Holm correction

***Mean value of positive pixels

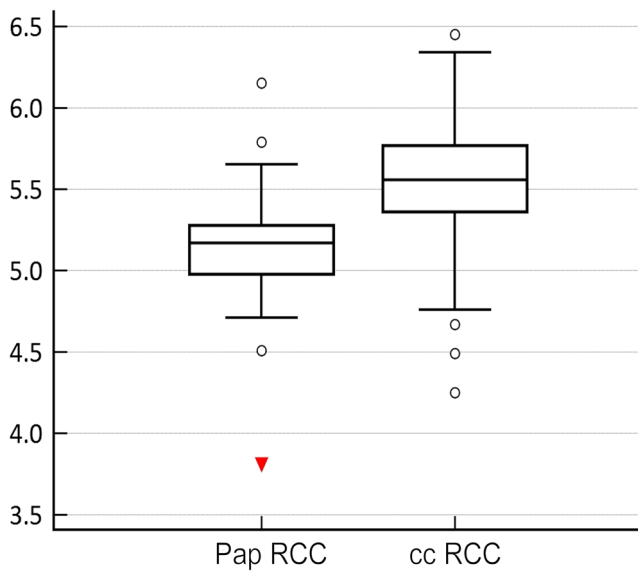


Fig. 3 Box and whisker plot of entropy values for papillary (pRCC) and clear cell (ccRCC) renal cancers at medium spatial scaling filter (SSF = 4). Pap RCC, papillary-type renal cell carcinoma; ccRCC, clear cell-type renal cell carcinoma. Boxes represent interquartile range. Central line in the box is the median value. Whiskers represent range of all values. Small circles and triangles refer to outliers. Note that the boxes of the two groups of RCC do not overlap

this context, CTTA may be more objective than visual analysis to assess heterogeneity inside an RCC. Consistent with previous studies, tumor size also demonstrates significant correlation with Fuhrman grade [49, 50]. Therefore, increased intratumoral heterogeneity (entropy) and large tumor size are risk factors for high-grade malignancy.

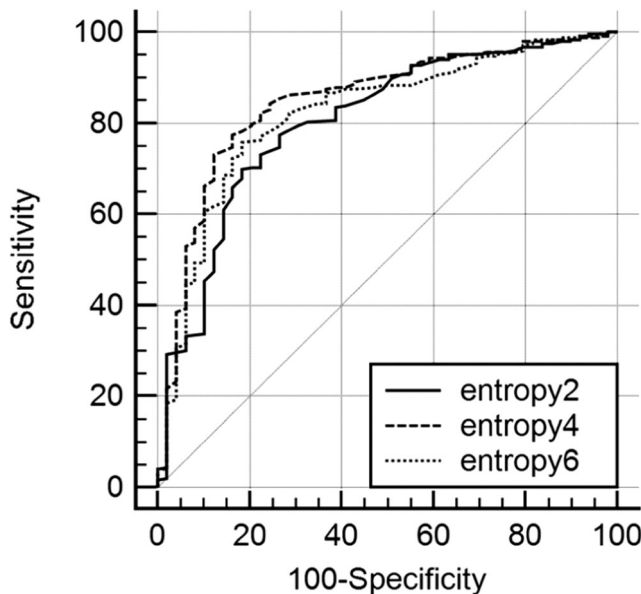


Fig. 4 ROC curves plotting sensitivity (y-axis) and 1-specificity (x-axis) of entropy at different spatial filters in differentiating ccRCC from pRCC. Entropy 2, entropy at fine spatial filter (SSF = 2 mm); entropy 4, entropy at medium spatial filter (SSF = 4 mm); entropy 6, entropy at coarse spatial filter (SSF = 6 mm). Area under ROC curves (AUC) are given in the text

We are aware of limitations of our study. Our study was retrospective. We had only one CTTA reviewer in this study. However, prior CTTA studies have shown good to excellent interobserver agreement [48, 51–54]. We used a single axial slice of tumor to assess CTTA, rather than using a three-dimensional approach. The latter would have been time consuming to do in large cohort. It has been shown that two-dimensional texture analysis gives adequate results, though multi-slice volume analysis may be more representative of tumor [55]. Selection bias toward high-grade, larger tumors may have been introduced due to the need for histopathologic confirmation in the study design. Smaller tumors, especially in older patients, may not necessarily undergo surgical excision. The prognostic ability of Fuhrman tumor grading for pRCC remains unclear currently due to conflicting evidence [56, 57]. Nevertheless, in routine urological practice, Fuhrman grading continues to be used. Finally, only two of the CTTA parameters tested achieved statistical significance for discrimination of ccRCC from pRCC, with *p* values that approached the cutoff of less than 0.05. This was mainly due to the robust post hoc Holm correction that was employed to reduce type I errors [31].

Establishing a more sophisticated and automatic tumor border tracking method is a promising future direction for this research to enable full evaluation of the volumetric heterogeneity of the tumor. We did not perform high-order statistics such as gray-level co-occurrence matrix (GLCM), gray-level run-length (GLRL), gray-level gradient matrix (GLGM), and Laws’ features [16, 35]. The first-order texture analysis performed in this study, however, was easy to implement and spatially invariant. Several studies prove that first-order parameters correlate to underlying physiological changes. The correlation between higher order texture analysis-derived parameters with pathophysiological changes remains unknown, although a recent study shows the diagnostic performance of first-order CTTA is more accurate than higher order CTTA in the differentiation of renal tumors [16].

In conclusion, CTTA is a promising modality for evaluation of renal tumors. CTTA may have utility for discrimination of tumor subtype, and for prediction of aggressive phenotypes. Entropy at fine and medium spatial scaling filters was able to differentiate ccRCC from pRCC with high specificity and sensitivity. Large tumor size and increased entropy correlate with high Fuhrman grade.

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Compliance with ethical standards

Guarantor The scientific guarantor of this publication is Kumaresan Sandrasegaran, M.D.

Conflict of interest The authors of this manuscript declare no relationships with any companies whose products or services may be related to the subject matter of the article.

Statistics and biometry No complex statistical methods were necessary for this paper.

Informed consent Written informed consent was waived by the Institutional Review Board.

Ethical approval Institutional Review Board approval was obtained.

Methodology

- Retrospective
- Case-control study
- Performed at one institution

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