

Radiogenomics in clear cell renal cell carcinoma: Correlations between advanced CT imaging (texture analysis) and microRNAs expression

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Introduction & Objectives: A relevant challenge for the improvement of clear cell renal cell carcinoma management could derive from the identification of novel molecular biomarkers that could greatly improve the diagnosis, prognosis, and treatment choice of these neoplasms. In this study, we investigate whether quantitative parameters obtained from computed tomography texture analysis (CTTA) may correlate with the expression of selected oncogenic microRNAs (miRNA). To the best of our knowledge, a possible correlation between CT texture parameters and miRNAs expression in ccRCC was not investigated yet.

Materials & Methods: In a retrospective single-centre study, multiphasic computed tomography examination (with arterial, portal, and urographic phases) was performed on 37 patients with clear cell renal cell carcinoma and computed tomography texture analysis parameters such as entropy, kurtosis, skewness, mean, and standard deviation of pixel distribution were measured using multiple filter settings. These quantitative data were correlated with the expression of selected microRNAs (miR-21-5p, miR-210-3p, miR-185-5p, miR-221-3p, miR-145-5p). Both the evaluations (microRNAs and computed tomography texture analysis) were performed on matched tumour and normal corticomedullary tissues of the same patients cohort.

Results: In this pilot study, we evidenced that computed tomography texture analysis has robust parameters (eg, entropy, mean, standard deviation) to distinguish normal from pathological tissues. Moreover, a higher coefficient of determination between entropy and miR-21-5p expression was evidenced in tumour versus normal tissue. Interestingly, entropy and miR-21-5p show promising correlation in clear cell renal cell carcinoma opening to a radiogenomic strategy to improve clear cell renal cell carcinoma management.

CTTA Parameters and MiRNAs Pearson Correlation (Arterial Phase; SSF1.5).

	Mean	SD	Entropy	MPP	Skewness	Kurtosis
Normal tissue						
Δ (%) miR-21	0.30	-0.14	0.06	-0.10	-0.21	0.09
Δ (%) miR-210	-0.09	-0.26	0.23	-0.27	-0.28	-0.21
Tumor						
Δ (%) miR-21	-0.24	0.07	0.16	0.007	0.04	-0.09
Δ (%) miR-210	0.11	0.15	0.09	0.17	-0.01	-0.13

Abbreviations: CTTA, computed tomography texture analysis; MPP, mean of positive pixels; SD, standard deviation; SSF, spatial scaling factor.

Conclusions: This study for the first time showed a promising correlation between microRNAs and computed tomography texture analysis in clear cell renal cell carcinoma. The clear cell renal cell carcinoma can benefit from non-invasive evaluation of texture parameters (mean and entropy) in adjunction to liquid biopsy results. In particular, a promising correlation between entropy and miR-21-5p was found.