INTRODUCTION AND OBJECTIVE: Leibovich score has been a standard method to predict recurrences in renal cell carcinoma (RCC). Recently, Grade, Age, Nodes, and Tumor (GRANT) score was proposed as an alternative. The objective was to examine the performance of Leibovich score versus GRANT score in predicting disease recurrence.

METHODS: In total, 7,653 patients diagnosed with RCC from 2010 to 2018 were captured in the nationwide DaRenCa database; 2,652 underwent radical or partial nephrectomy and had full datasets regarding the GRANT score and Leibovich score. Discrimination was assessed with a Cox regression model. The results were evaluated with concordance index (C-index) analysis.

RESULTS: Median follow-up was 40 months (IQR 24–56). Recurrence occurred in 17%, and 15% died. Among 1,957 clear cell (cc) RCC patients the distribution of GRANT grant score of 0,1,2, or 3/4 was 21%, 56%, 21% and 1.4%, respectively, and for Leibovich score of low/intermediate/high this was 47%, 36% and 18%, respectively. A similar distribution was seen in 655 non-cc patients. Both Leibovich and GRANT scores performed well in predicting outcomes for the favorable patient risk groups. The Leibovich score was better at predicting RFS (C-index 0.736 vs 0.643), but not OS (C-index 0.657 vs 0.648). Median follow-up was 40 months (IQR 24–56). Recurrence occurred in 17%, and 15% died. Among 1,957 clear cell (cc) RCC patients the distribution of GRANT grant score of 0,1,2, or 3/4 was 21%, 56%, 21% and 1.4%, respectively, and for Leibovich score of low/intermediate/high this was 47%, 36% and 18%, respectively. A similar distribution was seen in 655 non-cc patients. Both Leibovich and GRANT scores performed well in predicting outcomes for the favorable patient risk groups. The Leibovich score was better at predicting RFS (C-index 0.736 vs 0.643), but not OS (C-index 0.657 vs 0.648).

CONCLUSIONS: GRANT and Leibovich score were validated in clear cell and non-clear cell RCC. Leibovich score outperformed the GRANT score in predicting RFS and should remain the standard approach to risk stratify patients during follow-up.

INTRODUCTION AND OBJECTIVE: Several prognostic models have been described for clear cell renal cell carcinoma (ccRCC). Some techniques used to evaluate molecular biomarkers are cost-prohibitive, thereby preventing widespread adoption for personalizing patients’ therapy. In this study, we profiled the urine for potential inflammation-related biomarkers in a cohort of patients with ccRCC and describe a model to predict overall survival (OS).

METHODS: Urine supernatants from 17 patients with ccRCC were prospectively collected before surgery. The concentrations of 96 analytes in urine supernatants were measured using a proximity extension analysis by OLink Proteomics™. Unsupervised clustering and differential protein expression analysis between clusters was performed. Genes encoding proteins that were found significantly differentially expressed between the clusters were evaluated for effects on OS by Kaplan Meier (KM) curves using the Cancer Genome Atlas (TCGA) dataset. We performed a logistic regression model using genes that were significantly associated with OS in KM analyses. Genes associated with worse OS were identified and risk groups were defined based on the number of risk factors present. Association between risk groups and OS was evaluated using a cox proportional hazard model.

RESULTS: We identified two distinct clusters based on the concentration of urinary proteins in our ccRCC cohort (Fig 1A). We identified 60 proteins significantly differentially expressed between them (Fig 1B). Patients bearing tumors with high expression of TWEAK, TNFSF14 and CCL7, and low expression of CX3CL1 were associated with worse prognosis in TCGA. We found that OS was significantly associated with the number of molecular risk factors present in these ccRCC tumors (Fig 2).

CONCLUSIONS: We observed distinct inflammatory signatures in a cohort of ccRCC patients. Expression of genes encoding a subset of these proteins that were differentially expressed between clusters...