

ASCO[®] Genitourinary
Cancers Symposium

Circulating KIM-1 and ctDNA as prognostic markers in oligometastatic clear cell renal cell carcinoma (ccRCC): The K-COMPASS model



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#GU26

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Key Takeaway Points

First analysis of KIM-1 within an oligometastatic ccRCC cohort

- KIM-1 measured at baseline and 3 months were associated with progression free survival, systemic therapy free survival, overall survival

First analysis of ctDNA and KIM-1 in the same cohort

- Baseline ctDNA and KIM-1 were independently associated with systemic therapy free survival

Kidney Cancer OligoMetastasis Prognostic Assessment Systemic Score (K-COMPASS model) integrates clinical features with ctDNA and KIM-1 to estimate systemic therapy free survival for oligometastatic ccRCC patients.

- <https://www.trialdesign.org/one-page-shell.html#K-COMPASS>

Background

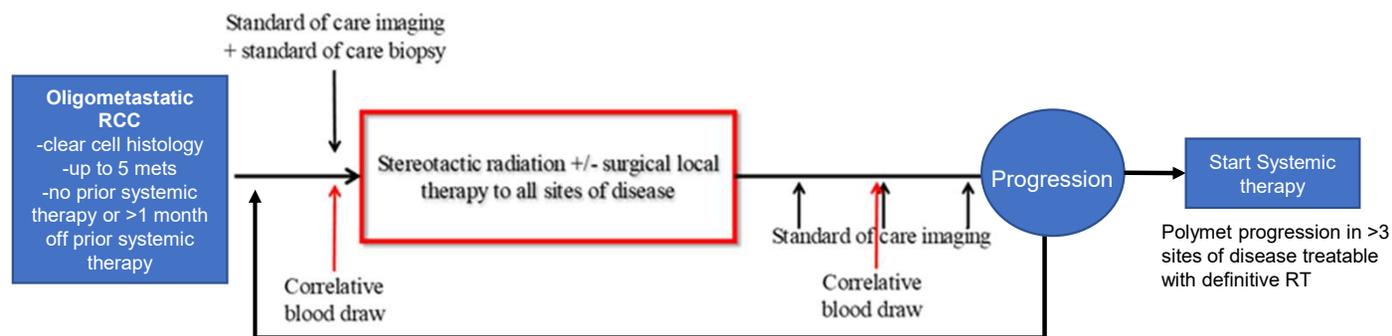
KIM-1

- Kidney Injury Molecule 1 (KIM-1) is a transmembrane glycoprotein expressed in normal kidney and RCC.
- Circulating KIM-1 is prognostic pre-nephrectomy, post-nephrectomy, and in metastatic RCC patients receiving systemic therapy.

ctDNA

- Circulating tumor DNA (ctDNA) is shed from malignancies and prognostic for outcomes across various cancer types.
- Its use has been limited in RCC given the low shedding phenotype of most RCC, the genetic heterogeneity in metastatic RCC, and its lower mutation burden

Methods



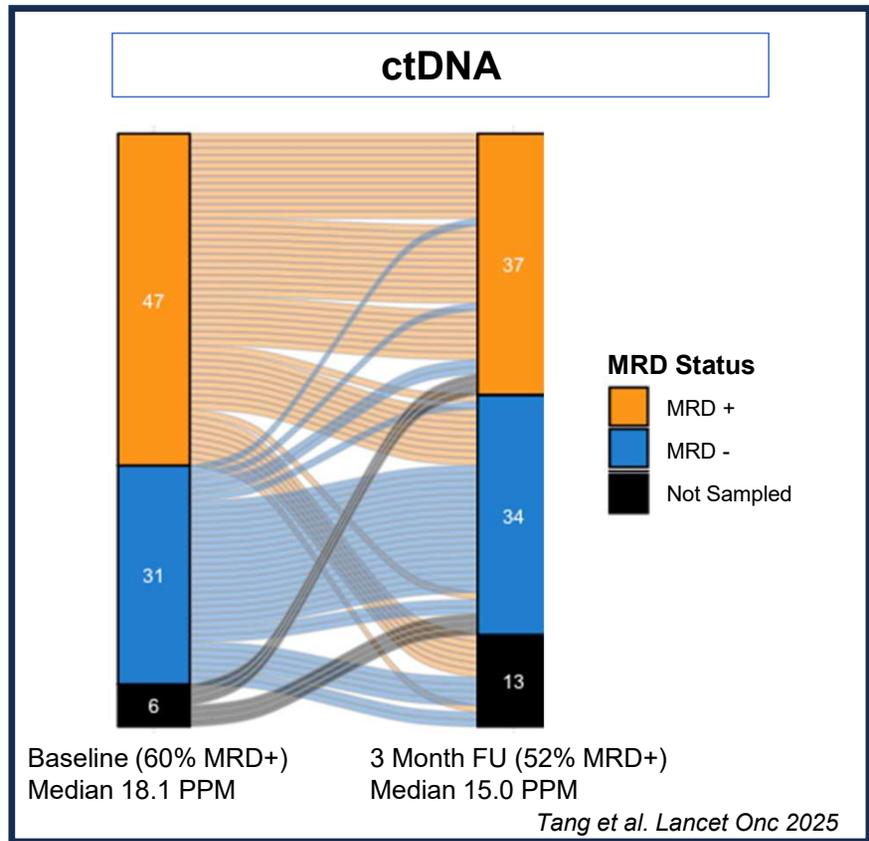
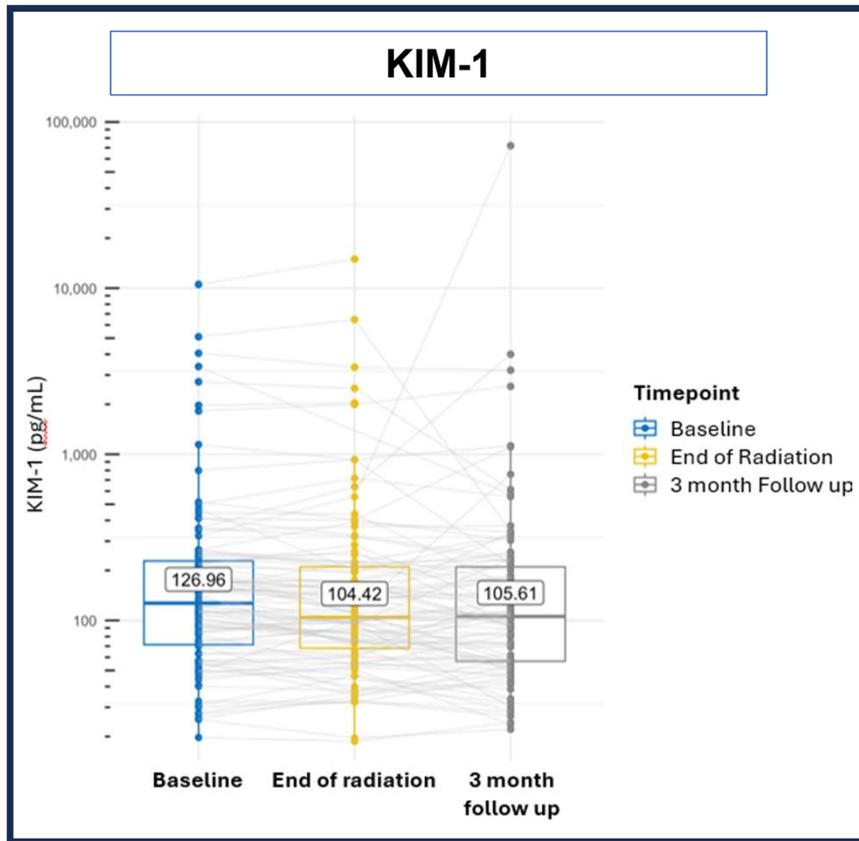
Patient Population:

- Phase II trial investigating metastasis directed radiation therapy without systemic therapy (*Tang et al. Lancet Onc 2025* and *Tang et al. Lancet Onc 2021*)
- 112/120 (93%) had **KIM-1** and 89/120 (74%) had **ctDNA**

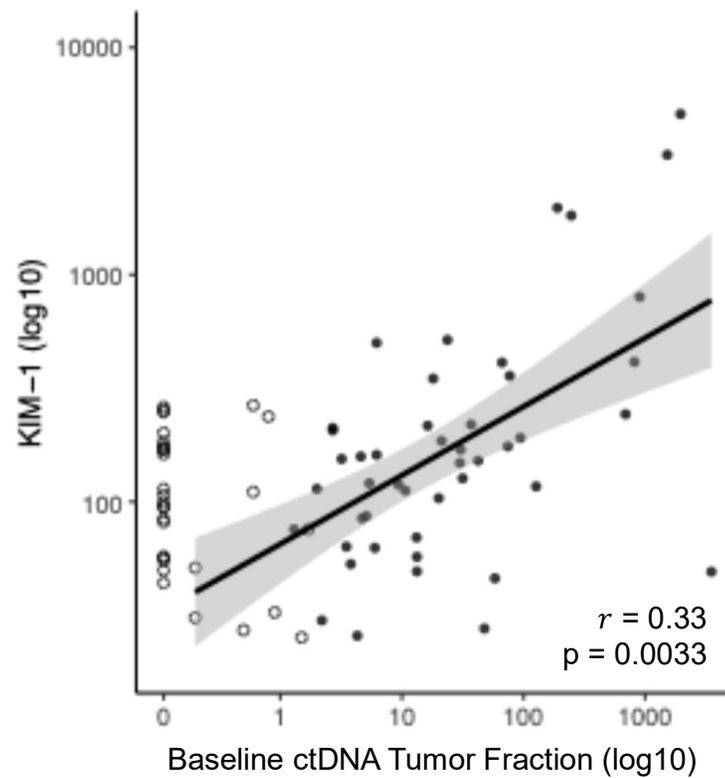
Assays

- ELISA-based assay to measure plasma **KIM-1** protein levels
- Customized **ctDNA** panels of ≤ 2000 somatic variants from WGS (Precise MRD, Myriad Genetics)

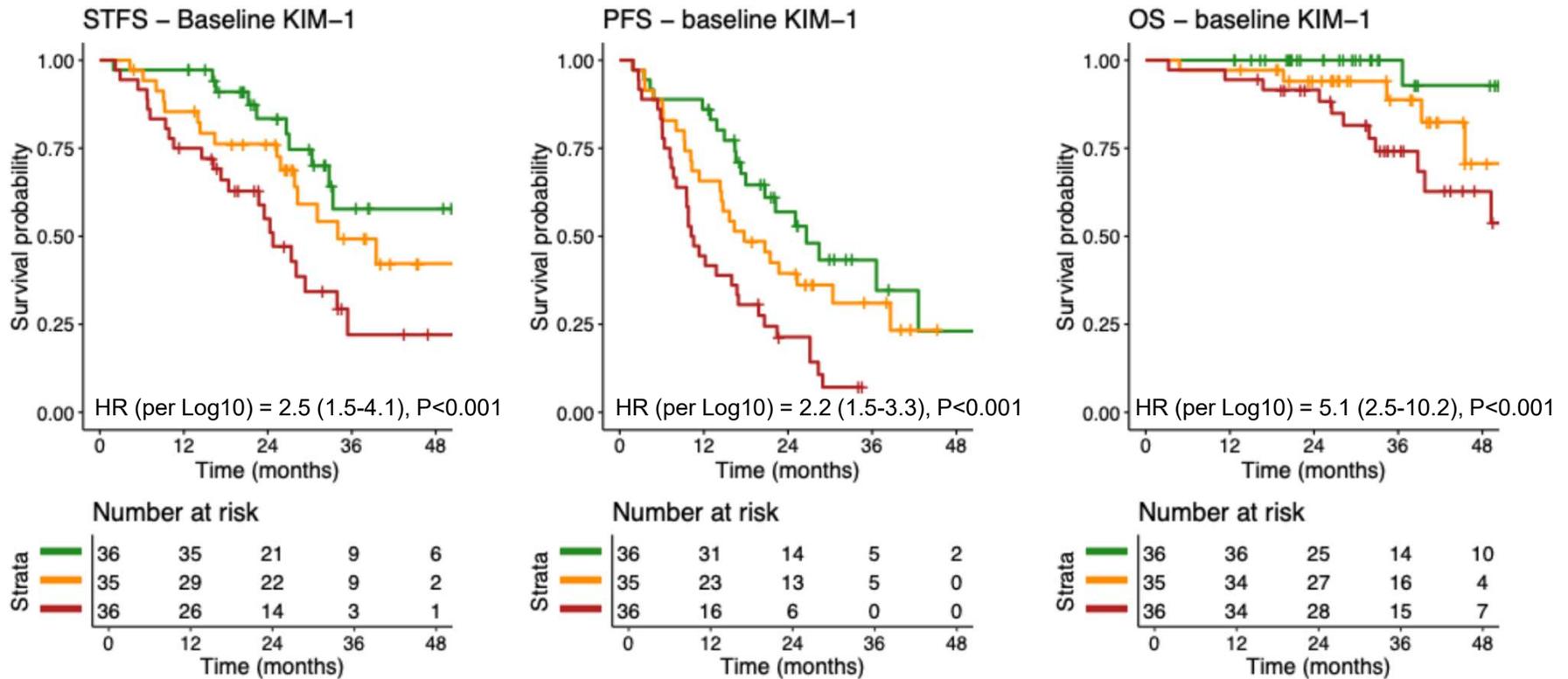
Results – Baseline Detection



Results – Baseline KIM-1 and ctDNA



Results – Baseline KIM-1 and outcomes



Results – Baseline KIM-1 and ctDNA

Parameter	Baseline		3-Month Follow-Up	
	Univariable	Multivariable	Univariable	Multivariable
KIM-1 (per log ₁₀ [pg/mL])	2.5 (1.5–4.1) P<0.001	1.9 (1.0–3.6) P=0.041	3.22 (1.91–5.43) P<0.001	2.22 (1.09–4.51) P=0.03
ctDNA (MRD+ vs MRD–)	2.8 (1.3–5.9) P=0.0089	2.47 (1.1–5.6) P=0.03	4.42 (2.09–9.50), P<0.001	2.70 (1.09–6.67) P=0.03

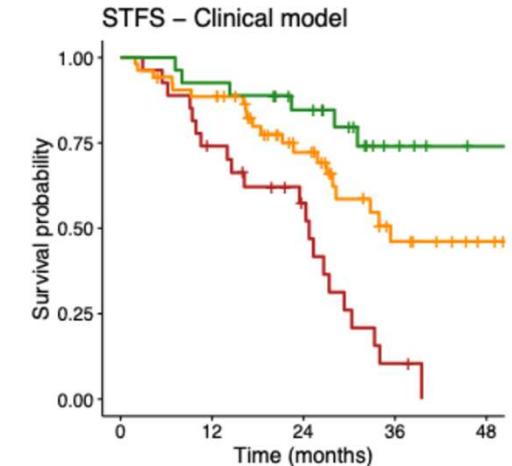
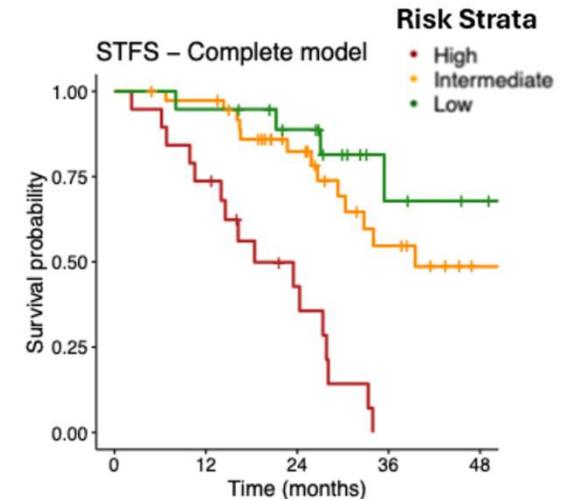


Results – K-COMPASS model

- Elastic net-based feature importance selecting top 6 out of 21 clinical variables.
- Final K-Compass model consisted of these 6 variables fit with Weibull regression
- K-Compass exhibited strong discrimination for STFS (C-index 0.76) and outperformed the clinical model (C-index 0.66)

Available at <https://www.trialdesign.org/one-page-shell.html#K-COMPASS>

		Parameters	Selection frequency
Clinical Model	K-COMPASS Model	KIM-1 (per log ₁₀ [pg/mL])	100%
		ctDNA MRD (MRD+ vs MRD-)	100%
		Prior lines of systemic therapy at baseline (per line)	100%
		Eastern Cooperative Oncology Group (ECOG) score (per 1 point)	66%
		Number of metastatic lesions at baseline (per 1 lesion)	66%
		Time from diagnosis to metastasis (per 1 month)	55%



Thank you

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