Whole genome cfDNA profiles reveal common signatures of immune checkpoint inhibition in kidney, melanoma, and lung cancers

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BACKGROUND

Whole genome cfDNA profiles reveal common signatures of immune checkpoint inhibition across multiple cancers, including non-small cell lung cancer (NSCLC), kidney cancer, and melanoma. To identify predictive biomarkers for patients undergoing ICI treatment, we applied gene set enrichment analysis (GSEA) to reveal characteristic gene expression patterns across the genome.

OBJECTIVE

To identify predictive biomarkers of ICIs response and explore molecular mechanisms of resistance in NSCLC, kidney cancer, and melanoma using cfDNA study.

METHODS

- Whole genome cfDNA profiles from 214 patients with NSCLC, kidney cancer, and melanoma were analyzed using GSEA.
- Gene set enrichment analysis (GSEA) was performed on weighted average effect sizes of TSS-GAP levels, with a significance threshold of q-value<0.05.
- To identify signatures with high confidence in predicting response, we applied Monte Carlo permutation tests and adjusted for multiple testing.

RESULTS

We identified characteristic gene expression patterns across the genome in NSCLC, kidney cancer, and melanoma patients undergoing ICI treatment. These patterns were enriched for hallmark gene sets related to cell cycle processing, JAK/STAT signaling, and DNA damage.

CONCLUSIONS

This study shows promising cfDNA signatures that may have potential use for patient stratification and response monitoring. This study highlights the potential of cfDNA as a non-invasive biomarker for ICI response.

REFERENCES


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