4-based second ICI therapy, with 4 (10%) having PR and one (2%) having CR of disease following second ICI-based treatment. Patients spent an average of 21.4 weeks on the second ICI regimen. The response rate for the entire cohort was 11.9% (16.7% for RCC and 0% for UC). The CR rate for the entire cohort was 40% (40% for RCC and 40% for UC). Immune-related adverse events were experienced in a subset of patients (28%).

Conclusions Although we observed a low OR rate to a second ICI-based regimen, a select subset of patients did have CR from a second ICI regimen. Current studies exploring the addition of CTLA4 inhibitors to anti-PD-1 therapy may provide insight into the greater efficacy of treatment within a subset of patients. Further analysis of a larger cohort receiving sequential immunotherapy is necessary to better identify patients who may be more likely to derive CR from sequential ICI.

Ethics Approval This retrospective study was approved by the Emory University Institutional Review Board.

Consent Not applicable

Acknowledgements Research reported in this publication was supported in part by the Breen Foundation.

Trial Registration Not applicable.

REFERENCES

Not applicable

http://dx.doi.org/10.1136/jitc-2020-SITC2020.0255

Clinical trials completed

DEVELOPMENT OF A DIAGNOSTIC PLATFORM WHICH MATCHES THERAPIES TO THE TUMOR MICROENVIRONMENT DOMINANT BIOLOGY

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Background Tumor microenvironment (TME)-targeting agents such as anti-angiogenic therapies and check-point inhibitors (CPIs), have shown both promise and variability in effectiveness depending on the tumor type. For immune-targeting agents like CPIs, efforts to identify features or biomarkers that predispose responding patients include but are not limited to genomic stability, tumor mutation burden, and PD-L1 expression. Oncology is developing a RNA-based platform that identifies subsets of patients based on multiple aspects of the biological processes (dominant biology) existing within the tumor microenvironment.

Methods RNA data from publicly available sources including microarray, RNASeq exome and whole RNA were analyzed with respect to gene signatures that describe four different microenvironmental phenotypes. Phenotypes were then evaluated for relationships to clinical efficacy endpoints. From these RNA signatures and driven by machine learning methodologies, drug-specific algorithms were developed and applied to retrospectively to clinical data. Comparative analyses were explored between gene signatures, commonly used biomarkers (eg. presence of microsatellite DNA, expression levels of PD-L1, etc) and within-patient metadata to better understand better how this approach can be utilized in prospective clinical studies.

Results Attributes in RNA expression identified using Oncology’s platform have retrospectively characterized responders to CPIs or anti-angiogenic drugs, demonstrating a relationship between clinical response and biomarker positive and negative patient populations. Exploratory data summarizing the use of this platform demonstrates its utility for enriching...