Poster 43: Evaluation of circulating tumor DNA using the Haystack MRD assay in recurrent ovarian cancer: a tale of four patients

Presenting Author: Vinita Popat, MD, City of Hope National Medical Center

Topic
Ovarian

Objectives
To assess the clinical utility of the Haystack minimal residual disease (MRD) tumor-informed circulating tumor DNA (ctDNA) assay for serial treatment monitoring in recurrent ovarian cancer.

Methods
Four patients with recurrent ovarian cancer (1 platinum-sensitive, 3 platinum-resistant; high grade serous n=3, clear cell n=1; 2nd–4th line therapy) were prospectively enrolled in a national multicenter study. Serial plasma ctDNA was collected every 3 weeks, aligned to treatment cycles and correlated with CA-125 and radiographic response. Haystack MRD employs whole genome sequencing (WGS)-informed, patient-specific variant panel design with proprietary error correction, achieving detection at tumor fractions as low as 0.0006%: among the lowest reported analytical limits of any commercially available ctDNA platform.

Results
ctDNA was detected in all patients at every timepoint, correlating with CA-125 in 3 of 4 cases. In the platinum-sensitive patient, both markers declined concordantly with clinical response. In a platinum-resistant patient on a clinical trial study drug, both fell initially then rose together, anticipating radiographic progression. In two cases, ctDNA provided utility beyond CA-125: one patient withdrew after two timepoints, yet ctDNA was detectable and rising despite a consistently normal CA-125, suggesting occult disease burden (with confirmed disease progression at a later time point); and in a patient with clear cell carcinoma, ctDNA was the sole dynamic biomarker while CA-125 remained static throughout, with stable disease on imaging.

Conclusions
This study represents one of the first prospective evaluations of a WGS-informed Haystack MRD ctDNA assay during active treatment for recurrent ovarian cancer. Universal ctDNA detection across all timepoints demonstrated dynamic kinetics that largely paralleled CA-125 trends, while in select cases provided earlier or complementary signals. These findings underscore the platform’s potential clinical utility, particularly in platinum-resistant and CA-125–non-secretory histologies. Patient accrual is ongoing, with the goal of generating sufficient prospective data to inform the design of a larger-scale trial evaluating WGS-informed ctDNA as a clinical decision-making tool in recurrent ovarian cancer.

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