Clinical utility of TP53 mutations (TP53m) dynamic monitoring in circulating tumor DNA (ctDNA) in patients (pts) with high-grade ovarian carcinomas (HGOC).

1 Oncology Department, Gustave Roussy Cancer Center, Villejuif, 2 Oncology Department, Hôpital Saint-Louis, Paris, 3 Oncology Department, Hôpital Européen Georges Pompidou, Paris, 4 Inserm UMR 881, Gustave Roussy Cancer Center, Villejuif, 5 Inviva Ltd, Babraham, Cambridge, UK.

BACKGROUND

Patients with HGOC enrolled in a prospective academic study (OnvBioMark,NCT03161214) consented to analysis of ctDNA samples obtained throughout the disease course (CT or MRI) to identify those who should benefit from maintenance treatment or therapy escalation to eliminate minimal residual disease.

OBJECTIVE

We assessed the clinical utility of TP53m in ctDNA for detecting minimal residual disease (MRD) and as a marker of early response to chemotherapy and early relapse.

MATERIALS AND METHODS

PATIENTS AND METHODS

Patients with HGOC enrolled in a prospective academic study (OnvBioMark,NCT03161214) consented to analysis of ctDNA samples obtained throughout the disease course - at diagnosis, after DS, during chemotherapy or at relapse.

cDNA was analysed using InVisionFirst® to detect the presence of SNVs, indels, and CNAs in 37 cancer-related genes, including TP53Hom in confirm presence of ctDNA.

Overall survival (OS) and Progression Free Survival (PFS) were estimated using Kaplan-Meier method in each group. A total of 37 patients with HGOC were included in the study. Median time of follow up was 42 months (range 27.7-101.9 months). At the time of analysis, 23 patients were still alive, 9 have never relapsed and are free of disease, 5 patients had no mutation at any time point, 140 samples from 37 pts with HGOC were collected at various time points during the disease course (Figure 1). ctDNA was identified in 132 samples (94.3%) samples, in 32 patients (86.4%) at any time point. Patients with HGOC enrolled in a prospective academic study (OnvBioMark,NCT03161214) consented to analysis of ctDNA samples obtained throughout the disease course (CT or MRI) to identify those who should benefit from maintenance treatment or therapy escalation to eliminate minimal residual disease.

RESULTS

A total of 37 patients with HGOC were included in the study. Median time of follow up was 42 months (range 27.7-101.9 months). At the time of analysis, 23 patients were still alive, 5 patients had no mutation at any time point, 9 have never relapsed and are free of disease, and 5 patients had no mutation at any time point. Patients with HGOC enrolled in a prospective academic study (OnvBioMark,NCT03161214) consented to analysis of ctDNA samples obtained throughout the disease course (CT or MRI) to identify those who should benefit from maintenance treatment or therapy escalation to eliminate minimal residual disease.

CONCLUSION

Our pilot study confirms the sensitivity and clinical utility of ctDNA monitoring in HGSOOC patients in several areas. The detection of TP53m in ctDNA after DS seems to be associated with poor outcome and its increase or appearance during neoadjuvant chemotherapy may predict failure to achieve complete DS. ctDNA can detect occult disease and preceded biological or radiological relapse by at least 6 months. In HGOC pts, TP53m in ctDNA could be used as an early surrogate marker of response to treatment, can help identify those who should benefit from maintenance treatment or therapy escalation to eliminate minimal residual disease.

REFERENCES


CONTACT

Maria KFOURY, MD. Has no conflict of interest

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