Introduction/Background Using clinically relevant imaging modalities in relevant animal models is crucial for strengthening the translational value of preclinical discoveries in endometrial cancer (EC). Imaging by 18F-fluorodeoxyglucose positron emission tomography/computed tomography (18F-FDG-PET/CT) is commonly used in diagnostic work-up in EC. 18F-FDG PET/CT in orthotopic mouse models of EC have been shown to be feasible, but standardized guidelines for image acquisition and interpretation is missing. Utilizing a large imaging database of orthotopic EC models, we aimed to characterize primary tumour 18F-FDG PET parameters and assess treatment response in a subset of mice.

Methodology The database consists of 91 18F-FDG-PET-CT scans in 66 mice orthotopically implanted with patient-derived xenografts (n=30) or organoid-based patient-derived xenografts (n=36). A subset of mice was used for evaluation of treatment response (n=25). The mice were fasted for 12–16 hours prior to imaging, intravenously injected with 18F-FDG and scanned for one hour. The following tumour parameters were extracted; max, mean and peak standardized uptake value (SUV<sub>max</sub>/SUV<sub>mean</sub>/SUV<sub>peak</sub>), metabolic tumour volume, total lesion glycolysis, the 10 hottest voxels and metabolic rate of FDG. Interreader reliability between two readers were evaluated using intraclass correlation coefficient (ICC) test (n=25).

Results We utilized a 50% of SUV<sub>max</sub> segmentation threshold for tumour delineation, which correlated well with anatomical tumour volume extracted from MRI for a subset of mice ($r^2=0.74$, n=25). There was a significant difference between treatment and control groups for the parameters SUV<sub>max</sub>(p=0.020), SUV<sub>peak</sub> (p=0.038) and the 10 hottest voxels (p=0.034) and the agreement between the readers were good (ICC; 0.89–0.97).

Conclusion 18F-FDG PET/CT in EC mouse models is feasible and multiple metabolic tumour features can be extracted. Using a clinically relevant imaging modality strengthens the potential for preclinical to clinical translation and reproducibility. Our work provides a basis for future studies on orthotopic mouse models of EC.
Conclusion Ngs can help classify rare diseases if the classical pathological diagnostics do not give a satisfying diagnosis. There are currently no clear treatment recommendations for STK11 adnexal tumors yet. International registries and solid clinical follow-up data are urgently needed to enhance our knowledge on these potentially aggressive tumors.

2022-RA-945-ESGO

ANTITUMOUR ACTIVITY OF DOSTARLIMAB BY PD-L1 AND TUMOUR MUTATION BURDEN IN PATIENTS WITH MISMATCH REPAIR DEFICIENT AND PROFICIENT TUMOURS IN THE GARNET TRIAL

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10.1136/ijgc-2022-ESGO.878

Introduction/Background Dostarlimab is a programmed death-1 (PD-1) inhibitor approved as monotherapy in patients with mismatch repair deficient (dMMR) recurrent/advanced endometrial cancer (EC) that has progressed on or after platinum-based chemotherapy or solid tumours that have progressed on or after prior treatment, with no satisfactory alternative treatment options. We report a post hoc analysis of antitumour activity by PD1L expression and tumour mutational burden (TMB) in patients with dMMR and MMR proficient (MMRp) solid tumours in the GARNET trial.

Methodology GARNET (NCT02715284) is a phase 1, multicentre, open-label, single-arm study of dostarlimab in patients with advanced/recurrent solid tumours. Three expansion cohorts enrolled patients based on MMR status: dMMR (A1) with advanced/recurrent solid tumours. Three expansion centre, open-label, single-arm study of dostarlimab in patients with dMMR (A2) with advanced/recurrent EC, and dMMR non-EC solid tumours (F). Patients received dostarlimab 500 mg IV Q3W for 4 cycles, then 1000 mg IV Q6W until progression or discontinuation. TMB and PD1L were exploratory biomarkers. TMB status was determined by FoundationOne test; TMB-high (TMB-H) was defined as ≥10 mutations/Mb. PD1L expression was determined by combined positive score (CPS) by Ventana assay; PD1L-high (PD1L-H) was defined as CPS ≥1. The study was not powered to assess antitumour activity within subgroups.

Results TMB-H and PD1L-H were common in dMMR solid tumours; PD1L-H was observed in 39.4% of MMRp EC tumours (table 1). Objective response rate (ORR) was higher in patients with TMB-H/PD1L-H tumours (55.6% for all cohorts, combined; Table). Safety for each cohort was previously reported.1

Conclusion PD1L-H and TMB-H were frequently observed in the dMMR EC and non-EC cohorts, regardless of tumour type; PD1L-H was also prevalent in MMRp EC tumours. Although not a powered analysis, ORR by BICR per RECIST v1.1 was higher in patients with TMB-H and PD1L-H solid tumours. Across cohorts, dMMR status was predictive of response.

REFERENCE


2022-RA-968-ESGO

IMMUNOTHERAPY RESPONSE MONITORING USING PERSONALIZED CIRCULATING TUMOR DNA ANALYSIS IN PATIENTS WITH RELAPSED GYNECOLOGIC MALIGNANCIES

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10.1136/ijgc-2022-ESGO.879

Introduction/Background Immunotherapy has transformed cancer care. Unfortunately, responses within gynecologic malignancies have been modest when compared to other disease sites. Biomarkers for early determination of treatment benefit are urgently needed to spare unnecessary toxicity and cost. We evaluated if circulating tumor DNA (ctDNA) dynamics enable early detection of progressive disease (PD) and treatment response in patients with recurrent, gynecologic malignancies receiving immunotherapy.

Methodology Longitudinal plasma samples (n=138) were collected from 25 patients with recurrent cervical (N=6), endometrial (N=12), or ovarian (N=7) cancers who received immunotherapy. A personalized, tumor-informed multiplex PCR assay (SignateraTM bespoke mPCR NGS assay) was used for the detection of ctDNA in plasma samples.

Results Pre-treatment samples were available for 9 patients (78% ctDNA detection rate) and all 25 patients had on-treatment samples (68% ctDNA detection rate). Serially ctDNA negative patients (3/15 with imaging) had no evidence of disease on-treatment. ctDNA clearance was observed in 3 (cervical, N=2; endometrial, N=1) of the remaining 12 patients and correlated with clinical benefit. ctDNA decreased in additional 2 patients, both with objective response, while all 7 patients with increased ctDNA had PD. Increased ctDNA