methylation were 67.2% and 89.6% in all CIN3+ subjects compared with HPV16/18 (68% and 66.4%) and LBC (≥ASCUS; 93.6% and 23.6%). The specificity of HPV 16/18 and CisCer methylation combined screening method were 96.1% in CIN3+. The CIN2, CIN3, and cancer immediate risk with combined screening method were 79.2%, 61.46%, and 26.04%, respectively.

Conclusion The preliminary results indicated that the CisCer testing is promised for cervical cancer detection with high sensitivity and specificity for hrHPV. It can be used as a new non-invasive diagnosis method and its utility as a second triage step after hrHPV testing in women with cervical lesions to improve the accuracy of referral colposcopy.

**2022-RA-911-ESGO** \(^{18}F\)-FDG-PET/CT IN ORTHOTOPIC MOUSE MODELS OF ENDOMETRIAL CANCER: MULTIPARAMETRIC CHARACTERIZATION AND EVALUATION OF TREATMENT RESPONSE

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Abstract 2022-RA-911-ESGO Figure 1

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 \(^{18}F\)-fluorodeoxyglucose positron emission tomography/computed tomography (\(^{18}F\)-FDG-PET/CT) is commonly used in diagnostic workup in EC. \(^{18}F\)-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 \(^{18}F\)-FDG PET parameters and assess treatment response in a subset of mice.

Methodology The database consists of 91 \(^{18}F\)-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 \(^{18}F\)FDG and scanned for one hour. The following tumour parameters were extracted: max, mean and peak standardized uptake value (SUV\(_{\text{max}}$/SUV\(_{\text{mean}}$/SUV\(_{\text{peak}}$), 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\(_{\text{max}}\) -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\(_{\text{max}}\) (p=0.020), SUV\(_{\text{peak}}\) (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 \(^{18}F\)-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.

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 tumors that have progressed on or after prior treatment, with no satisfactory alternative treatment options. We report a post hoc analysis of antitumor activity by PD1 expression and tumour mutational burden (TMB) in patients with dMMR and MMR proficient (MMRp) solid tumours in the GARNET trial.

METHODS GARNET (NCT02715284) is a Phase 1, multi-center, open-label, single-arm study of dostarlimab in patients with MMR status: dMMR (A1) centre, advanced/recurrent EC; and MMRp (A2) advanced/recurrent EC, and dMMR non-EC cohorts enrolled patients based on MMR status: dMMR (A1) centre, open-label, single-arm study of dostarlimab in patients with dMMR and MMR proficient (MMRp) advanced/recurrent EC (N=60). TMB-high (TMB-H) was defined as ≥10 mutations/Mb. PDL1 expression was determined by combined positive score (CPS) by Ventana assay; PD-L1-high (PD-L1-H) was defined as CPS ≥1. The study was not powered to assess antitumor activity within subgroups.

Results TMB-H and PD-L1-H were common in dMMR solid tumours; PD-L1-H was observed in 39.4% of MMRp EC tumours (table 1). Objective response rate (ORR) was higher in patients with TMB-H/PD-L1-H tumours (55.6% for all cohorts, combined; Table). Safety for each cohort was previously reported.

Conclusion PD-L1-H and TMB-H were frequently observed in the dMMR EC and non-EC cohorts, regardless of tumour type; PD-L1-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 PD-L1-H solid tumours. Across cohorts, dMMR status was predictive of response.


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 utility 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 (Signatera™ 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). Serial 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