an NGS panel, identifying challenges in case classification and possible solutions.

Methodology We performed the FoundationOne CDx NGS panel on 60 EC and assigned molecular subtype: *POLE* mutated (P*OLE*mut), mismatch repair deficient (MMRd), p53 abnormal (p53abn) or no specific molecular subtype (NSMP).

Result(s)* In 55 patients the molecular classification was successful. A pathogenic *POLE* mutation was detected in 9 cases (*POLE*mut). 20 were MMRd (12 MSI-high, 8 MSI-indeterminate based on the NGS panel MSI classifier) and a known or likely MMR gene mutation was found in 7 of these. Of the remaining 26 cases, 17 carried a *TP53* mutation (p53abn) and the remaining 9 were considered to be NSMP. The tumor mutation burden (TMB) was significantly different ($p<0.001$) in the molecular subtypes (A) and high TMB (>55 mut/MB) was 100% specific for *POLE*mut EC ($p<0.001$). High TMB was specific for known pathogenic *POLE* mutations and was not elevated in cases with solely non-pathogenic *POLE* mutations (B).

In non-*POLE*mut cases, TMB was higher in MSI-high and MSI-indeterminate than microsatellite stable (MSS) cases (C), and a TMB of >7 mut/MB was 100% specific for MMRd EC. There was one MSS EC with a TMB of 18 mut/MB but it showed loss of MLH1 and PMS2 proteins on immunostaining and was classified as MMRd.

Conclusion* An NGS panel can be used in the molecular classification of EC when there is sufficient tumor cellularity. TMB can be used as an adjunct in molecular subtype diagnosis for tumors that are difficult to classify. Additionally, TMB can potentially serve as a diagnostic adjunct in cases with POLE mutation of unknown significance.

1012 THE ROLE OF GENITAL TRACT MICROBIOTA CONTINUUM IN ENDOMETRIAL MALIGNANCY

[1;2]A Semertzidou*, [1]D Macintyre, [1]J Marchesi, [1;2]P Bennett, [1;2;3]M Kyrgiou. [1]*Imperial College London, Metabolism, Digestion and Reproduction, London, UK*; [2]*Queen Charlotte's and Chelsea- Hammersmith Hospital, Imperial Healthcare NHS Trust, London, UK*; [3]*Imperial college London, Metabolism, Digestion and Reproduction, London, UK*

10.1136/ijgc-2021-ESGO.223

Introduction/Background* Endometrial cancer has a dominant place among gynaecological cancers and is the fourth most common malignancy in women. Accumulating reports have associated gynaecological precancer and cancer with dysbiotic microenvironments. Our aim was to identify a microbial signature in endometrial cancer and explore its role in disease pathogenesis.

Methodology Eligibility criteria included patients undergoing total abdominal/laparoscopic hysterectomy for endometrial cancer or benign indications. Microbiome swabs were collected along the female genital tract (FGT) (vagina, external cervical os, endometrium, fallopian tubes and ovaries) and rectum. The V1-V2 hypervariable regions of 16S rRNA genes were sequenced (Illumina MiSeq platform), data were analysed with Mothur software package and OTU taxonomies were determined. Benign and malignant endometrial organoids were cultured and treated with increasing concentrations (10%, 20%, 30%) of *L. crispatus*- conditioned media. Proliferation was assessed by the CellTiter-GLo® 3D cell viability assay and cytokine/chemokine secretion (IL-1β, IL-1ra, IL-2, IL-6, IL-8, IL-10, G- CSF, GM- CSF, IFN-γ, TNF-α, CCL4/MIP1beta, CCL5/RANTES) by the Magnetic Multiplex Cytokine Array (R&D systems).

Result(s)* Sixty-one women were recruited; 37 had endometrial cancer and 24 were benign controls. We confirmed the presence of a genuine, low– abundance microbiome above background contamination in the endometrium, fallopian tubes and ovaries in a subset of benign and endometrial cancer patients, which was one- four orders of magnitude lower than the heavily colonised vagina, cervix and rectum. In 75% (12/16) of benign patients, we found that the most abundant species of the lower genital tract could also be recovered from the whole length of the upper genital tract, while the microbial continuum was less cohesive in endometrial malignancy. We also demonstrated that *Lactobacillus* depletion and high microbial diversity along the genital tract are characteristic in endometrial cancer patients with concurrent enrichment of *Porphyromonas*, *Prevotella, Peptoniphilus* and *Anaerococcus*. Different histotypes and grades of endometrial cancer were not marked by microbial differences. *L.crispatus*, a FGT commensal that is depleted in endometrial cancer, was shown to reduce viability of endometrial cancer organoids at high concentrations and impact on cytokine secretion by benign and malignant endometrial organoids.

Conclusion* Endometrial cancer displays a distinct microbial signature. *L.crispatus* may exert an anti- proliferative effect in endometrial cancer and interfere with inflammatory pathways.

1019 INTERIM ANALYSIS OF 10-YEAR DATA REGARDING TREATMENT AND PROGNOSIS OF UTERINE CARCINOSARCOMA CASES ACROSS THE THAMES VALLEY CANCER ALLIANCE NETWORK

[1]SL Smyth*, [2]A Gkorila, [3]A Mcculloch, [4]P Tupper, [2]A Sattar, [2]N Sadeghi, [2]S Spencer, [2]K Zarrindej, [2]V Le Thanh, [2]J Rencher, [2]G Sharma, [2]A Kashif, [2]M Abdalla, [1]S Addley, [5]S Siddiki, [2]M Alazzam, [2]H Soleymani Majd. [1]*Churchill Hospital, Gynaecological Oncology, Oxford, UK*; [2]*John Radcliffe Hospital, Oxford, UK*; [3]*Royal Berkshire Hospital, UK*; [4]*Stoke Mandeville Hospital, UK*; [5]*Great Western Hospital, UK*

10.1136/ijgc-2021-ESGO.224

Introduction/Background* Uterine Carcinosarcoma (UCS) comprises <5% of uterine malignancies, accounting for >15% associated mortality. With no established guidelines, we present our experience to determine optimal treatment and prognosis of UCS.

Methodology We conducted a multicentre retrospective cohort study, including all surgically managed UCS cases between March 2010 and January 2020. Data was collected on FIGO staging and post-operative management, recurrence and survival outcomes.

Result(s)* 82 (9.7%) UCS cases were identified. Table 1 demonstrates case staging and management strategies. 23 patients underwent surgery alone due to poor performance status, comorbidities, age or treatment refusal. 15.8% had lymph nodes metastases, which was in keeping with the literature. Recurrence occurred in 47.8% and 77.8% of cases of early and late stage respectively; most frequently in the pelvis, but also commonly in the pelvic lymph nodes and chest. Both recurrence and subsequent death usually occurred within the first 1-2 years following treatment. This retrospective analysis explores for significance in overall and disease free survival between disease stage groups and treatment modalities using univariable and multivariable Cox regression models and Kaplan-Meier curves.