before treatment. Paired sample analysis before and after treatment showed that imiquimod acts on the PD-1/PD-L1 pathway, decreasing PD-1 expression (P= 0.0155) in cases of successful treatment (figure 1), possibly controlling the inflammation. We observed that PD-1 levels were not correlated with PD-L1 levels (p=0.5177).

Conclusion Our results suggested that imiquimod modulates PD-1 expression in cervical lesions and that treatment success depends on PD-1 levels at admission. In contrast, increased PD-L1 expression is associated with a higher risk of unsuccessful treatment.

Disclosures The authors report no conflict of interests.

#931 CLINICAL IMPLICATIONS OF SPATIAL INTRA-TUMOURAL HETEROGENEITY ON HOMOLOGOUS RECOMBINATION DEFICIENCY SCORES IN HIGH GRADE SEROUS OVARIAN CANCER

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Introduction/Background High-grade serous ovarian cancer (HGSOC) is typified by extensive genomic instability and intra-tumoural heterogeneity (ITH). Most patients relapse and eventually acquire resistance to platinum- or PARP inhibitor-based therapy. Diverse mechanisms leading to therapy resistance and lack of predictive biomarkers means that matching the best treatment options to patients is difficult. This study aims to examine the effect of temporal and spatial ITH in advanced stage HGSOC on homologous recombination (HR) deficiency scores at presentation and relapse and implications for patient management.

Methodology Patients (n=45) at Hammersmith Hospital (HH) undergoing maximal-effort upfront cytoreduction for advanced HGSOC underwent mapping of their tumour dissemination and tumour biopsies collected (range 4–15). Paired relapse samples were collected for 10 patients. Tumour DNA was extracted (n=5 tumours per patient, plus relapse tumours) and Illumina Human OmniExpress genotyping performed. Allele-specific copy number (CN) was quantified using ASCAT. Multi-site CN data was also accessed from two cohorts (GSE38787, GSE40546). HR scores were estimated in each cohort using a genomic scar (GSE38787, GSE40546). HR scores were estimated in each cohort using a genomic scar algorithm, applying a 'scarHRD' algorithm, applying a cut-off ≥ 42 for HR-deficient (HRD).

Results Variations in HR scores were observed across the cohorts with a proportion of patients presenting with a mixed HR score, displaying both HRD and HR-proficient (HRP; <42) scores in their tumours: HH cohort (22%, 10/45 patients); GSE38787 (17%, 4/24 patients); and GSE40546 (28%, 4/14 patients). In the HH cohort, we examined if mixed HR status was associated with survival and demonstrated that patients with mixed HR status or all HRP tumours had poorer progression-free (p>0.0052) and overall survival (p=0.00092) than patients with all HRD tumours.

Conclusion Variations in HR-deficiency/proficiency scores indicates HR status may be inconsistent in advanced disseminated HGSOC, thus suggesting that a single tumour biopsy may not accurately depict spatial HGSOC tumour biology.

Disclosures None to declare

#1051 LIQUID BIOPSY BASED DETECTION OF HUMAN PAPILLOMAVIRUS IN CERVICAL CANCER AND CERVICAL DYSPLASIA PATIENTS

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Introduction/Background Cervical cancer (CC) is the 4th most commonly diagnosed cancer among women, leading to approximately 528,000 new cases annually. Current screening approaches for this disease have certain limitations; Pap tests require dedicated cytopathology infrastructure, while human papillomavirus (HPV) DNA testing may lead to invasive procedures in patients with transient infection. Liquid biopsy has emerged as a minimally invasive approach to detect and monitor disease. We and others have previously demonstrated the clinical utility of circulating tumor (ct)DNA to monitor HPV+ cancers. However, little is known about the presence of ctDNA from different liquid biopsy analytes in CC patients.

Methodology The aim of this study was to compare the presence of HPV-ctDNA isolated from different liquid biopsy analytes in patients with CC and cervical dysplasia (CD). Blood, urine, and vaginal swabs were collected from 23 patients with CC (adenocarcinoma or squamous cell carcinoma) and 22 patients with CD at the McGill University Health Centre. Of these patients, longitudinal samples pre- and post-treatment were collected in 7 patients. DNA was extracted using a commercial kit and tested for ctDNA by digital droplet PCR for HPV16, 18 and 33.

Results HPV16, 18 or 33 ctDNA was found to be detectable 14/23 (60%) CC samples and 2/22 (9%) CD patients in plasma, urine, and/or vaginal swab. Concordance in ctDNA positivity across sample types was seen in 90% of cases. Major reductions (97.7–100%) were seen in ctDNA concentrations in all analytes in CC patients following treatment.

Conclusion HPV-ctDNA was detectable in all liquid biopsy analytes sampled in patients with CC and CD, with a higher frequency of detection in CC samples. Treatment led to reductions in ctDNA across analytes in cancer patients. Globally, this data points to HPV ctDNA analysis as a promising method for detecting and monitoring HPV-related CC and CD.

Disclosures The authors have no disclosures

#1076 PROGNOSTIC FACTORS OF BREAST CANCER IN YOUNG FEMALE PATIENTS: A RETROSPECTIVE STUDY FROM SOUTHERN-EAST TUNISIA

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Introduction/Background Breast cancer (BC) is rarely seen in young women, but recent data shows an increase in rates