less than 200 at the time of death. Six of them had 3 separate malignancies.

Conclusions: Median age at time of diagnosis was significantly lower than that of the general population. HIV-infected women are at high risk for HPV-associated malignancies, even those who respond to antiretroviral therapy as measured by high CD4 levels and low viral loads. Multiple concurrent cancers are relatively common, even in patients with well-controlled HIV. Based on the data, survival was strongly correlated with response to antiretroviral therapy. However, multiple confounding factors may be present, emphasizing the need for further study. Careful cancer surveillance is critical and should be maintained, even in women who are responding to antiretroviral therapy. Similarly, oncologic encounters provide opportunities to reinforce the importance of adherence to antiretroviral therapy. Additionally, once a diagnosis of malignancy has been made, the level of vigilance in screening for other malignancies should increase.

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Poster #26

Focal Adhesion Kinase (FAK) Regulation of Programmed Death-1 (PD-1)/Programmed Death Ligand-1 (PD-L1) checkpoint signaling in a mouse model of epithelial ovarian cancer

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Objectives: Our objectives were to create an aggressive mouse ovarian cancer model with genetic similarity to human high grade serous ovarian cancer (HGSOC); and to use this model to explore the effect of focal adhesion kinase (FAK) on tumor cell proliferation, leukocyte infiltration, and expression of PD-1 and PD-L1.

Methods: We previously derived the aggressive "ID8-IP" mouse ovarian cancer cell line from ID8 cells by intraperitoneal passage into an immunocompetent C57BL/6 mouse. Exome sequencing was used to determine deletions and copy number alterations (CNAs), and RNA sequencing was used to determine relative gene expression between the ID8 and ID8-IP cell lines. A FAK knockout cell line was generated ("ID8-IP FAK KO") using the CRISPR/Cas9 system, and a third cell line ("ID8-IP FAK re-expressing") was created by re-introducing FAK into "ID8-IP FAK KO" cells using lentiviral transduction. Tumor cells were injected intraperitoneally into C57BL/6 mice (n=8 per group), and tumor cell and immune cell populations among ascites-associated cells were identified using flow cytometry.

Results: Our ID8-IP cell line demonstrated several deletions and CNAs analogous to common genomic alterations in human HGSOC (Table 1). In particular, there were several alternate splice variants in the tumor suppressor p53 gene (Trp53), and no p53 protein detected in the ID8-IP cell line by Western blot. Using our mouse model, we found a higher proportion of tumor cells in the ID8-IP compared to the ID8-IP FAK KO (61.4% vs 24.4%, respectively; $p<0.0001$), and fewer leukocytes (19.9% vs 48.3%, $p=0.0003$). There were more PD-1 positive CD8+ T cells in the ID8-IP relative to the ID8-IP FAK KO (38.18% vs 14.26%, respectively; $p=0.038$). Similar trends were noted between the ID8-IP FAK re-expressing and ID8-IP FAK KO groups. In vitro, ID8-IP cells had more cell surface PD-L1 expression compared to ID8-IP FAK KO cells (81.4% vs 39.7%, respectively; $p<0.0001$), with the highest PD-L1 expression in the ID8-IP FAK re-expressing cells (88.5%).

Conclusions: We established a unique mouse ovarian cancer model with genetic similarity to human high grade serous ovarian cancer that allows for study of the immune microenvironment. Here, we present a novel link between FAK and the PD-1/PD-L1 pathway in ovarian cancer. Ongoing studies will further explore the relationship between FAK and this immune checkpoint pathway, as well as other immune cell populations.

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Poster #27

Incidence and implications of circulating tumor cells in endometrial cancer

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Objectives: Endometrial cancer is the most common gynecologic malignancy affecting women in the United States. Historically, 20-25% of patients with clinical stage I disease will have extrauterine disease at the time of surgery. These patients account for a large proportion of endometrial cancer related recurrences and deaths. Recently, the utility of surgical staging has been called into question by a series of prospective trials that have failed to demonstrate a survival benefit for comprehensive surgical staging. Currently, no biomarker exists to predict which patients are at risk for extrauterine disease at the time of presentation. Increasing numbers of circulating tumor cells (CTCs) have been linked to the ability to predict metastases in malignancies like breast cancer. This study aims to evaluate the ability of CTCs to serve as a biomarker for identifying women at risk of metastatic disease and need for comprehensive surgical staging.

Methods: A prospective cohort study was performed. Informed consent was obtained and 10mL of whole blood was collected from women with clinical stage I endometrial carcinoma of any tumor grade and histology. The CTCs were collected from the sample using an ISET device, fixed in duplicate on a porous membrane, stained with MGG, and identified and counted by a gynecologic pathologist. Clinical, demographic, and outcome data was abstracted from patient's electronic medical records. Summary statistics were used to describe demographic and clinical characteristics. Fisher's Exact Tests were used to assess associations between CTCs and clinical variables.

Results: 37 patients with clinical stage I endometrial cancer were included in the study. The majority of patients (59.5%, n=22) had IA disease following definitive surgical management. Eleven patients (29.7%) were found to have extrauterine disease following surgery. CTCs were identified in 48.7% of patients. There was no association between FIGO stage and presence of CTCs ($p=0.5621$). There was no association between tumor grade and presence of CTCs ($p=0.6092$). Additionally, there was no association between tumor histology and presence of CTCs ($p=0.6943$).

Conclusions: CTCs do not appear to be a reliable indicator of extrauterine disease among women with clinical stage I endometrial cancer. Further study is needed to develop predictive markers for those women requiring comprehensive surgical staging in this population.

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Poster #28

Vitamin D, leptin, vitamin D receptor single nucleotide polymorphism and treatment-related morbidity in ovarian, primary peritoneal, and fallopian tube cancer

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Objectives: Vitamin D deficiency confers poor outcomes in many cancers. While little data exists regarding the relationship between vitamin D deficiency and ovarian cancer (OC), the vitamin D receptor (VDR) single nucleotide polymorphism (SNP), FokI, is associated with increased OC risk. The relationship between the VDR FokI SNP and circulating serum 25 hydroxycholecalciferol (25(OH)D) is unknown. While vitamin D aids in production of inflammatory hormones such as leptin, the relationship between leptin and 25(OH)D levels in OC patients (pts) has not been studied. This study aimed to characterize 25(OH)D levels at the time of OC diagnosis and its associations with treatment-related morbidity, leptin levels, and VDR SNP status.
Methods: A retrospective review was performed of pts diagnosed with OC treated at a single institution. Pts were grouped by serum 25(OH)D status, with 25(OH)D deficiency defined as < 20 ng/mL and insufficiency 20-29 ng/mL. Demographics, clinical characteristics, treatment-related morbidity, survival, serum 25(OH)D, leptin, and VDR SNP markers were compared between groups.
Results: Of 122 pts included in the study, 82 were 25(OH)D deficient, 21 were insufficient, and 19 were normal. The median age was 67 yrs, and 70% were stage III/IV. There were no differences in demographics, stage, treatment-related morbidities or survival between groups (all p>0.05). There was no difference in serum leptin levels or SNP allele status between groups (all p>0.05). Due to differences in severity of disease and expected disease outcomes, further analysis was restricted to those with stage III/IV OC (n=85, deficient n=59, insufficient n=13, normal n=13). For this cohort, there was no difference in demographics, treatment-related morbidities, or survival (all p>0.05). When adjusted for BMI, there was no difference in serum leptin levels between groups or SNP allele status (all p>0.05, Table). There was no association between SNP allele groups and progression free (p=0.44) or overall survival regardless of 25(OH)D status (p=0.96).
Conclusions: This study did not detect an association between serum 25(OH)D levels and treatment-related morbidity, leptin levels, or VDR SNP status in women with OC in either the overall population or only those with stage III/IV disease. Interpretation is limited by small numbers and the retrospective design. Few patients receiving neoadjuvant chemotherapy were included in this study likely introducing selection bias. Prospective evaluation is ongoing.

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Poster #29

Family history of cancer associated with improved survival in uterine serous carcinoma

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Objectives: Uterine serous carcinoma (USC), a subset of endometrial cancers, accounts for fewer than 10% of cases, but disparately accounts for 50% of uterine cancer related deaths. Prior reports indicate an association between USC and BRCA 1 germline mutations. Our objective was to compare the survival of patients with USC with and without a family history of breast, ovarian, uterine, GI, pancreatic, brain, melanoma or GU cancers (Multiple Organ Hereditary Cancers or MOHC).
Methods: We extracted all genetic alterations in the commonly tested genes during genetic panel testing, progression free survival (PFS), and overall survival (OS) from The Cancer Genome Atlas (TCGA) in all patients with USC. We performed a multi-institutional retrospective review of all patients who were diagnosed with USC from 2005 to 2014. Demographics and clinic-pathologic data were obtained. Disease progression was defined by RECIST criteria. Statistical analysis was performed using the Kaplan-Meier Survival Analysis.
Results: Genetic alterations in the following commonly tested genes were extracted from TCGA in USC patients: BRCA1, BRCA2, CHEK2, BRIP1, RAD51C, BARD1, TP53, RAD50, RAD51D, ATM, NBN, PALB2, MRE11A, MSH6, MLH1, MSH2, PMS2. In those with advanced (stage III/IV) USC (n=69), PFS and OS were worse in patients with a genetic alteration of the above genes versus those without (PFS of 47.7 versus 19 mos and OS of 50.9 versus 30.1 mos; P = 0.01). One hundred ninety patients with USC were included in the retrospective analysis. Greater than 50% of the patients had a personal and/or family history of MOHC. 30% of these patients had a personal history of MOHC. When comparing survival between those with and those without a personal and/or family history of MOHC, patients with a MOHC history had longer PFS (49 versus 20 mos, P = 0.01) and longer OS (65 versus 34 mos, P = 0.01). Although not significant, a difference in overall survival was seen among patients with advanced USC (n=104) with a personal and/or family history of MOHC versus those without (35 versus 20 mos, P = 0.16).
Conclusions: Women with USC with a personal and/or family history of MOHC have improved survival compared to those without. Identification of genetic predisposition may improve treatment options and outcomes in this subgroup of patients. Genetic testing should be considered in patients with USC.

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Poster #30

Chromobox 2 protein identified as driver of anoikis-escape and disease progression in high grade serous ovarian cancer

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Objectives: Chromobox 2 (CBX2), a polycomb repressor complex subunit, plays an oncogenic role in a variety of cancers. In prostate cancer, CBX2 is a driver of metastatic progression. We sought to investigate the hypothesis: CBX2 upregulation promotes advanced high grade serous ovarian carcinoma (HGSOC) by promoting a stem-like transcriptional profile and inhibiting anoikis.
Methods: Gene Expression Omnibus (GEO) and The Cancer Genome Atlas (TCGA) were queried to establish CBX2's role. In vitro evaluation of CBX2 occurred in PEO1, OVCAR8, and OVCAR4 HGSOC cell lines. PolyHEMA-coated plates forced cells to grow in suspension and simulated anoikis-escape. Quantitative polymerase chain reaction and immunoblots evaluated CBX2 expression. Small hairpin RNAs (shRNAs) knocked down CBX2 for loss-of-function studies. To mimic HGSOC progression several culture conditions (2D, colony formation, and 3D, spheroid) were examined. Secreted luciferase (gLuc) activity was utilized as a proliferation indicator. Stemness was tested with the Aldefluor assay, measuring aldehyde dehydrogenase activity (ALDH). Using patient tumors from the Gynecology Tissue and Fluid Bank (GTFB) and a HGSOC tissue microarray (TMA) with matched primary, metastatic, and lymph nodes, a CBX2 expression profile was established. Student's t-test was used to define statistical significance, with a p value of < 0.05.
Results: GEO/TCGA analyses established CBX2 is upregulated in HGSOC tumors compared to benign tissues and CBX2 expression conveyed worse disease-free survival (11.7 vs 17.6 months, Log-rank test p-value < 0.005) and overall survival (34 vs. 44.8 months, Log-rank test p-value <0.005). PEO1, OVCAR8 and OVCAR4 cells upregulate CBX2 when grown in suspension compared to adherent conditions. CBX2 knockdown led to a significant inhibition of proliferation in all culture conditions. Forced suspension promoted increased ALDH