public hospitals or satellite clinics may provide the support necessary to achieve equivalent cancer outcomes at outreach programs.

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Poster #15

Novel germline cyclin dependent kinase 4 variant as a suspected driver mutation for high-grade serous ovarian epithelial cancer

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Objectives: To analyze the role of a novel cyclin dependent kinase 4 (CDK4) variant of uncertain significance as a potential driver mutation in high grade serous epithelial ovarian cancer (HGSOC) and to demonstrate the utility of precision medicine for the translational management of gynecologic oncologic disease.

Methods: We extracted DNA from samples provided by a patient with recurrent ovarian cancer and performed whole exome sequencing (WES) at a depth of 150 million germline and 300 million tumorreads. To identify single nucleotide, insertion, deletion and splice site alterations we utilized a Genome Analysis ToolKit bioinformatics pipeline and computational engine to align, call and annotate germline and genomic alterations. Filtering with a threshold Combined Annotation Dependent Depletion (CADD) score > 15 identified suspected pathologic variants. Immunohistochemical (IHC) staining of tumor tissue for phosphorylated retinoblastoma (Rb) protein was performed using Phospho-Rb (Ser807/811). In vitro molecular modeling systems with peptide 2A self-cleaving polycistronic gene expression vectors in epithelial ovarian cancer cell lines (CaOV-3, OV-90 and SK-OV-3) were used to elucidate the genetic mechanisms governing tumor progression.

Results: WES identified a germline missense alteration in cyclin dependent kinase 4 (CDK4) (n.108 C>T). Sanger sequencing confirmed this alteration; and CADD analysis generated a score of 24, implicating this change as a likely pathologic driver variant. CKDK4 along with CDKN2A function to regulate cell cycle progression via phosphorylation of the tumor suppressor gene, retinoblastoma (Rb). Consistent with predicted models, IHC demonstrated upregulated inactivating phosphorylation of Rb at Ser807/811. In vitro studies clarifying the regulatory dysfunction of CDK4, n.108C>T, and the therapeutic use of CDK4 inhibitors with polycistronic molecular modeling of the CDKN2A/CDK4/Rb regulatory axis in epithelial ovarian cancer cells lines are ongoing.

Conclusions: CDK4 V37M is a novel germline variant that is highly likely to be a pathogenic driver mutation in this patient's HGSOC. Identification of this putative mutation could have important therapeutic implications as CDK4 inhibitors have been shown to have promising biologic activity in ovarian cancer cell lines. This translational investigation demonstrates the value of precision medicine to inform therapeutic decision-making for gynecologic cancers.

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Poster #16

Racial disparities in women with stage IIIC and IV epithelial ovarian cancer receiving neoadjuvant chemotherapy versus primary debulking surgery - A National Cancer Database study

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Objectives: Our objective is to use data from the National Cancer Database (NCDB) in order to determine if African American and Hispanic women are more likely to receive neoadjuvant chemotherapy (NACT) than primary debulking surgery (PDS), when compared to their white counterparts, since the much debated European trials showed that NACT was not inferior to PDS.

Methods: A retrospective cohort study was performed using data originating between the years of 2010-2014 from women with stage IIIC or IV epithelial ovarian cancer. Only women of white, African American, and Hispanic ethnicities were included, and all individuals were identified to have received either neoadjuvant chemotherapy or primary debulking surgery. Descriptive statistics were computed, and continuous variables were assessed for normality. Groups were compared using ANOVA or non-parametric medians tests for continuous variables, and chi-squared tests were used for dichotomous or categorical variables. A logistic regression was then used to identify if predictors of treatment. A P-value of 0.05 was identified to be statistically significant.

Results: A total of 19,889 women with stage IIIC and IV epithelial ovarian cancer were identified to have received NACT or PDS, and identified themselves as either white, African American, or Hispanic. A total of 15,024 (75.5%) were treated with PDS, while 4,865 women (24.5%) were treated with NACT. Of those treated with NACT, 24.5% were white, 27.0% were African American, and 22.1% were Hispanic ($p= 0.005$). When adjusting for age, facility type, facility location, payer source, income, education level, comorbidity score, histology, grade, and tumor size, being African American was a predictor of receiving NACT with an adjusted odds ratio (95% CI) of 1.308 (1.120-1.528). Although 30-day mortality rates did not vary significantly amongst the three groups (p 0.386), the 90-day mortality rates were significantly different for white, African American, and Hispanic women (2.0% vs 2.9% vs 1.6%, $p=0.013$). When comparing NACT to PDS, the 30-day and 90-day mortality rates were highest in the NACT group (1.1% vs 0.2%, $p<0.001$ and 2.7% vs 1.9%, $p<0.001$).

Conclusions: Neoadjuvant chemotherapy is being used in almost 25% of women with stage IIIC and IV epithelial ovarian cancer, but this treatment course is associated with worse 30-day and 90-day mortality rates. Evidence suggests that being African American is a predictor of receiving NACT.

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Poster #17

Depth of bowel invasion in ovarian cancer is not associated with worse outcomes

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Objectives: The FIGO staging consensus agreement from 2012 indicates that bowel mucosal involvement for epithelial ovarian cancer (EOC) should be assigned to stage IV disease. Finding no evidence for this recommendation, we examined the impact of recto-sigmoid colonic invasion on survival based on depth of invasion.

Methods: Patients having recto-sigmoid resection to achieve complete gross resection for stage IIIC/IV EOC between 2003 and 2011 were included. For this study, mucosal involvement was not considered stage IV. Degree of bowel invasion was defined as: serosal/subserosal vs. muscularis/submucosa/mucosa. Patients with only mesenteric involvement were excluded. Intraperitoneal disease (IP) dissemination patterns were defined as pelvic, lower abdomen, upper abdomen, and miliary disease. Comparisons between groups were evaluated using the log-rank test for progression free and overall survival (PFS, OS) and the chi-square test for IP dissemination pattern.