Abstracts

EP003/#1114  IDENTIFICATION OF MOLECULAR TARGETS AND PATHWAYS FOR IMPROVING ENDOMETRIAL CANCER RACIAL DISPARITIES

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Objectives Identify proteins present at significantly different levels in endometrial cancer specimens across 4 racial groups to direct future therapy.

Methods Proteins from endometrioid endometrial cancer specimens of women who self-identified as Black, American Indian, or White (N=12 each), or Asian (N=10) were measured by Tandem Mass Tag liquid chromatography-tandem mass spectrometry. Patients were matched for age and body mass index. Significant differences in protein levels were identified by ANOVA after adjustment of the first principal component and evaluated by Ingenuity Pathway Analysis. Drug effects on human Ishikawa endometrial cancer cells were evaluated using an MTT assay.

Results The only patient characteristics significantly different across racial groups were higher rates of diabetes in Blacks and hypertension in Whites. Fifty-eight proteins exhibited significant differences across all groups. The most significant pathways identified to be regulated by proteins significantly different in non-Whites compared to Whites are regulators of protein synthesis. Trametinib and 2-deoxyglucose inhibition of mitogen-activated protein kinase 3 and hexokinase-2, which were significantly upregulated in specimens from Blacks compared to Whites, reduced growth of endometrial cancer cells with half-maximal inhibitory concentrations of 3 uM and 3 mM, respectively, but did not interact synergistically.

Conclusions This study demonstrated significantly different protein expression profiles in endometrioid endometrial cancers across 4 races. These proteins represent candidate biomarkers and drug targets for development of strategies to improve disparate outcomes of endometrial cancer patients.

EP004/#741 DNA METHYLATION LANDSCAPE AS A POTENTIAL PLAYER IN ACQUIRED-DRUG RESISTANCE IN OVARIAN CANCER

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Objectives Development of therapeutic resistance is a major cause of mortality in high-grade serous ovarian cancer (HGSOC), thus a better understanding of acquired resistance mechanisms is needed. This study aimed to investigate how epigenomic events might be associated with acquired-drug resistance in HGSOC patients.

Methods Methylation and gene expression differences between primary platinum-sensitive (n=32) and recurrent acquired-resistant samples (n=28) was explored using a HGSOC dataset. High resolution melting was used to validate results using epithelial ovarian cancer cell lines and HGSOC tumours. A CRISPR-Cas9 approach was used to investigate the effects of DNA methylation editing in vitro. Plasma samples from HGSOC patients (n=17) and age-matched healthy controls (n=20) were used to investigate longitudinal methylation dynamics via droplet digital PCR.

Results Comparison of methylation and gene expression analysis identified several genes, known to be involved in diverse immune and chemoresistance-related pathways, that significantly differentiated between paired platinum-sensitive and acquired-resistant HGSOC samples, with three genes displaying the most consistent methylation changes (PDCD1, NKAPL, APOBEC3A). A CRISPR-Cas9 approach was used to interrogate the effects of APOBEC3A and NKAPL promoter methylation editing on platinum sensitivity, with demethylation of NKAPL promoter being associated with increased platinum sensitivity. Hypermethylation of NKAPL and APOBEC3A were detected in 46% and 69%, respectively, of plasma samples from women with relapsed HGSOC.

Conclusions Promoter methylation has been identified as potentially involved in HGSOC drug resistance. Further research is warranted to understand the future use of these methylation patterns as prognostic/predictive markers in the OC clinical setting.

EP005/#572 EXPLOITING SMARCA2 DEPENDENCY FOR TARGETED THERAPY IN SMARCA4-DEFICIENT OVARIAN CANCERS

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Objectives Most ovarian cancer (OC) patients recur after first-line treatment and develop chemoresistance, highlighting an unmet need for precision medicine in OC. Half of OCs harbor mSWI/SNF chromatin-remodeling complex alterations including 10% in the SMARCA4 gene. Studies to date have suggested that the catalytic subunits of the mSWI/SNF complex, SMARCA2 and SMARCA4, exhibit paralog dependency and thus present an opportunity for synthetically lethal molecular targeting. The aim of this study is to investigate SMARCA2-dependency in SMARCA4-deficient OCs and to identify synthetic lethal interactions of SMARCA2–protein degradation in these cancers.

Methods Using CRISPR-Cas9 lentiviral-transduction targeting the SMARCA4 gene, we developed novel murine syngeneic/isogenic OC cell lines from well-characterized cell lines ID8 and UPK10, and novel electroporation-based genetically engineered mouse model-derived cell line 3_1. Human isogenic