Introduction Circulating tumor cells (CTCs) have received enormous attention as a novel biomarker in various malignant diseases. The aim of this study was to evaluate CTC detection using tapered-slit membrane filter based chipsets in differential diagnosis of ovarian tumors.

Methods A total of 230 preoperative women with an indeterminate ovarian tumor were prospectively enrolled. Seven patients diagnosed with other primary origin and 20 patients sampled after neoadjuvant chemotherapy were excluded from the analysis. Sensitivity, specificity, accuracy, and area under the receiver operating characteristic curve (AUC-ROC) of CTC detecting chipsets were analyzed according to postoperative pathologic results respectively.

Results 81 (39.9%) benign tumors, 32 (15.8%) borderline tumors, and 90 (44.3%) ovarian cancers were pathologically confirmed. CTC detecting chipsets had sensitivity, specificity, accuracy, and AUC-ROC of 75.6%, 58.0%, 67.3%, and 0.655 (95% confidence interval [CI], 0.570–0.740) for differentiating ovarian cancer from benign ovarian tumor. Sensitivity, specificity, accuracy, and AUC-ROC for detecting ovarian cancer from borderline tumor were 75.6%, 50.0%, 68.9%, and 0.622 (0.505–0.739), respectively. In addition, sensitivity, specificity, accuracy, and AUC-ROC were 68.9%, 58.0%, 64.5%, and 0.622 (0.540–0.703) for differentiating borderline and malignant ovarian tumor from benign tumor. Sensitivity, specificity, accuracy, and AUC-ROC for detecting ovarian cancer from benign to borderline tumor were 75.6%, 58.0%, 67.3%, and 0.655 (0.570–0.723), respectively.

Conclusion/Implications Our study suggests that preoperative high-throughput viable CTC isolation using tapered-slit membrane filter based chipsets could have a potential role in differentiating ovarian malignancy from benign and/or borderline tumors.

EP007/#793

THE MECHANISM THAT AFFECTS CELL DEATHS FOR TUMOR SUPPRESSION GENE-PTEN BY EZH2 ACTIVITY IN A CERVICAL CANCER CELL LINE (HELA-R) WITH RADIATION-TREATMENT RESISTANCE

To identify differentially expressed genes (DEGs) and signaling pathways in cisplatin-resistant endometrial cancer (EC) cells.

Methods Cisplatin-resistant endometrial cancer cells were established through continuous treatment of endometrial cancer cells (RL95–2 and Ishikawa) with gradually escalating doses of cisplatin. RNA-seq was performed on both original and cisplatin-resistant EC cells to evaluate DEGs. Gene-set enrichment analysis (GSEA) was also performed to find biologic processes or pathways in relation to cisplatin resistance.

Results Common hallmark gene sets enriched in both cisplatin-resistant RL95–2 and Ishikawa include inflammatory response, epithelial-mesenchymal transition, and KRAS signaling up. Common DEGs include EMP3, CD70, and SERPINE1 in the inflammatory response gene set; LAMA2, BDNF, OXTR, CDH2, VIM, MATN3, ABL1BB, EDIL3, EMP3, CXCL1, SERPINE1, and IL32 in the epithelial-mesenchymal transition gene set; PTPRR, MMD, and KCNN4 in the KRAS signaling up gene set.

Conclusion/Implications We identified DEGs and several pathways enriched in cisplatin-resistant EC cells as potential therapeutic targets of cisplatin resistance, which need further validation.
**Introduction** Human endogenous retroviruses (HERVs) are suggested to be involved in the development of certain diseases, especially cancers. In pancreatic cancer cells, shRNA-mediated downregulation of HERV-K Env RNA decreases cell proliferation and tumor growth through the RAS-ERK-RSK pathway; in colorectal cancer, CRISPR-Cas9 knockout (KO) of the HERV-K env gene affects tumorigenic characteristics through the nupr-1 gene.

**Methods** To elucidate the function of HERV-K Env protein in cancers, HERV-K env gene was knocked out using CRISPR-Cas9 in ovarian cancer cell lines SKOV3 and OVCAR3. Tumorigenic features like cell proliferation, migration, and invasion were analyzed, as well as related protein expression via western blotting. Gene expression patterns were evaluated using next-generation mRNA sequencing and gene ontology and pathway analyses.

**Results** After HERV-K env gene KO, RNA and protein expression significantly decreased, and tumorigenic features like cell proliferation, migration, and invasion significantly reduced. RB protein expression significantly increased in HERV-K env KO SKOV3 cells, while phospho-RB protein decreased in OVCAR3 cells. Transcriptome analysis showed significant differences in 37 DEGs out of 4,325 DEGs. SKOV3 cells had 31 upregulated and 32 downregulated DEGs, mainly related to RNA splicing, aging, and angiogenesis genes. OVCAR3 cells had 226 upregulated and 1,464 downregulated DEGs, mainly related to RNA splicing and aging genes.

**Conclusion/Implications** The results of this study showed that HERV-K env gene KO affects cell proliferation, invasion, and migration of ovarian cells through RB and Cyclin B1 proteins, but the specific regulation pattern can differ by cell line.

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**EP010/#59 INSUFFICIENT SERUM APOLIPOPROTEIN A1 IMPAIRS ANTITUMOR RESPONSE OF CD8+ T CELL VIA HIF-1A-GLYCOLYSIS PATHWAY**

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**Introduction** The immunosuppressive microenvironment plays an important role in the occurrence and development of tumors. Studies have shown that ApoA1 insufficiency is closely related to tumor development, but the underlying mechanisms are not well understood.

**Methods** Serum lipids in endometrial cancer and ovarian cancer patients were compared. Then tumor models in ApoA1 transgenic mice, and in vitro experiments were used to identify the immunomodulatory roles and potential mechanisms of ApoA1 on CD8+ T cells.

**Results** Serum ApoA1 significantly decreased among the lipid parameters in patients with endometrial cancer and ovarian cancer compared to healthy controls. In endometrial cancer tissues, compared to ApoA1 deficiency group, ApoA1 insufficiency group showed an immunosuppressive state, manifested as increased CD163+ macrophages and decreased CD8+ T cell infiltration. Consistently, tumor-bearing A1KO mice also showed impaired tumor-infiltrating CD8+ T cell infiltration and function. Further CD8+ T cell depletion experiments confirmed that CD8+ T cells were required for the antitumor activity of ApoA1. In vitro, ApoA1 peptide L-4F can directly potentiate the antitumor activity of CD8+ T cells via HIF-1α-mediated glycolysis pathway. Mechanistically, we found that ApoA1 reduced the ubiquitination degradation pathway of HIF-1α by down-regulating FIH1, further maintaining the stability of HIF-1α protein and signaling activation. Lastly, tumor-bearing A1TG mice showed significant sensitivity to anti-PD-1 therapy, with retarded tumor growth and increased tumor necrosis.

**Conclusion/Implications** Our data demonstrated the critical roles of ApoA1 in remodeling immune microenvironment and enhancing CD8+ T cell immune functions via HIF-1α-mediated glycolysis, which supports the clinical investigation for a combination of ApoA1 supplementation and anti-PD-1 therapy in tumors.

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**EP011/#717 PREDICTION OF CHEMOTHERAPY RESPONSE WITH LIQUID BIOPSY OF BODY FLUID FROM PATIENTS WITH GYNECOLOGIC CANCER**

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**Introduction** Organoids are three-dimensional in vitro culture systems. This model has been shown to be superior to conventional two-dimensional cell culture in recapitulating functionality, architecture, and genomic features of tissues seen in vivo. Patients with gynecologic cancers, especially with refractory disease status, may experience the accumulation of malignant effusion fluids. In this study, accumulated body fluids were analyzed to predict chemotherapy response by using organoids culture systems.

**Methods** We obtained tumor specimens in the form of multicellular spheroids present in malignant effusion fluids. We developed organoid growth of tumor cells and used them as a platform for empirical drug sensitivity testing. Body fluid samples (either ascites or pleural effusion) from 44 patients with gynecologic cancers were collected. Multicellular spheroids were recovered and subjected to culture conditions designed to support organoid growth. Drug sensitivity testing with various chemotherapeutic agents was performed on these specimens.

**Results** Our model demonstrated organoids formed within days of primary culture. Established organoid lines showed patient-tumor dependent morphology and disease characteristics, recapitulating the features of patient-specific malignant cancers. Drug sensitivity testing identified several agents with therapeutic potential and these results displayed patient-specific sensitivity to different chemotherapeutic agents.

**Conclusion/Implications** Establishment of organoid culture of multicellular spheroids from gynecologic malignant effusions can be used as a platform for empirical drug sensitivity testing. These models may be helpful in screening new or existing therapeutic agents prior to individualized treatment options.