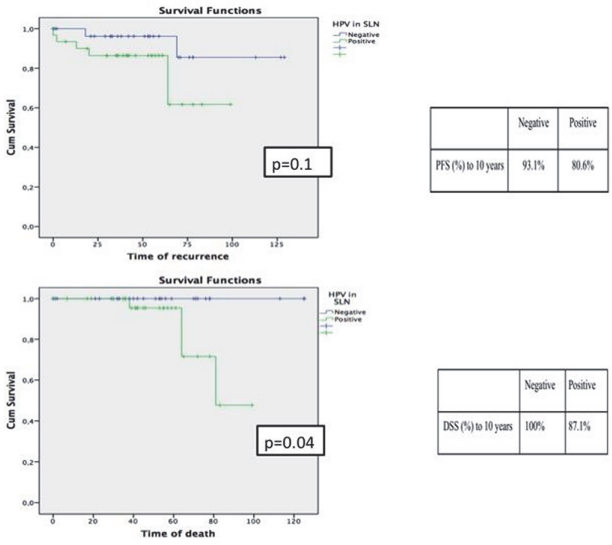
respectively 43.5 and 29.2 month, but, these differences are not statistical significant.However, all of the 4 deaths listed in our study occurred in the positive HPV DNA SLN group for which the 10 years Overall survival (OS) is thus significantly decreased.



	Negative	Positive
PFS (%) to 10 years	93.1%	80.6%

	Negative	Positive
DSS (%) to 10 years	100%	87.1%

Abstract 2022-RA-1480-ESGO Figure 1

Conclusion Our results show worst OS in patients with detected HPV DNA compared to patients without detected HPV DNA in their SLN and the same tendency is observed for PFS without significance. Thus, HPV DNA in SLN detected by ultrasensitive ddPCR could represent an interesting prognosis biomarker in N0 ECC.

2022-RA-1502-ESGO MULTIPLEXED BIOMARKER DETECTION USING THE QUANTIGENE ASSAY IN WOMEN LIVING WITH HIV FOR CERVICAL DYSPLASIA DETECTION

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Introduction/Background Cervical cancer (CxCa) and its precursor lesions are caused by persistent infection with a high-risk(HR) Human Papillomavirus (HPV). Women living with HIV (WLWH) have a higher risk for cervical dysplasia and CxCa development. The high HPV prevalence in WLWH makes a HPV-PCR based screening non-efficient. Biomarker detection could be a possibility, to find woman at risk. We evaluated the biomarker-based QuantiGene-Molecular-Profiling-Histology assay (QG-MPH) in WLWH.

Methodology We analysed a representative subset of samples (n=301) from the prospective 2H-study including HIV+ and HIV- women. A cervical sample was collected using a cyto-brush and fixed into ThinPrep/PreservCyt. The QG-MPH assay is based on the multiplexed Luminex bead-based technology platform (QuantiGene 2.0). It detects and quantifies the mRNA of 18 HR-HPV genotype-specific oncogenes, reference genes and cellular biomarkers including proliferation, tumour stem cell and tumour markers to predict the dysplasia stage, simultaneously.

Results HIV coinfection was significantly associated with increased mRNA expression of the following biomarkers in HR-HPV+ women without cervical lesions: leading HPV-E7 (p=0.0019), p16 (p=0.022), STMN1 (p=0.0039), MCM2 (p=0.015), KRT7 (p=0.0035) and KRT17 (p=0.014). In cervical cancer cases (HIV+=19, HIV-=18) only the expression of Nanog mRNA was different (p=0.022). Using the risk score developed on a HIV- cohort led to false positive detection (CIN3+) of 68.8% (n=22) in WLWH without lesions. Logistic regression analyses showed best markers for CxCa detection in HIV+ patients in our cohort were BIRC5, KRT17, MMP7 and p53 with a combined AUC of 0.93 (sensitivity=95%, specificity=82.0%).

Conclusion Viral oncogene expression is increased in HR-HPV + WLWH without cervical lesions. Biomarker evaluation has the potential to overcome problems of HPV PCR-based screening in WLWH. However, risk score adaptation is needed as biomarker expression varies between HIV+ and HIV- patients. Further studies with higher sample number are warranted to confirm the best markers and risk scores by QG-MPH analysis.

2022-RA-1558-ESGO A COMBINATION OF MOLECULAR AND CLINICAL PARAMETERS PROVIDES A NEW STRATEGY FOR HIGH-GRADE SEROUS OVARIAN CANCER PATIENT MANAGEMENT

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Introduction/Background High-grade serous carcinoma (HGSC) is the most common and deadly subtype of ovarian cancer. Although most patients will initially respond to first-line treatment with a combination of surgery and platinum-based chemotherapy, up to a quarter will be resistant to treatment. We aimed to identify a new strategy to improve HGSC patient management at the time of cancer diagnosis (HGSC-1LTR).

Methodology Ready-available formalin-fixed paraffin-embedded HGSC tissues obtained at the time of diagnosis were selected for proteomic analysis. Clinical data, treatment approach and outcomes were collected for all patients. Chemoresistant (TFIp < 6 m) and chemosensitive (TFIp > 6 m) groups were evaluated using discovery proteomics (discovery cohort, n=21). Protein candidates were verified in an independent cohort using targeted proteomics (verification cohort, n=88). Predictive analysis combined with a cross-validation was used to select those proteins able to correctly classify patients into chemoresistant and chemosensitive groups. The classification performance of the protein and clinical data combinations were assessed through the generation of receiver operating characteristic (ROC) curves.

Results Using the HGSC-1LTR strategy we have identified a molecular signature (TKT, LAMC1 and FUCO) that combined with ready available clinical data (patients' age, menopausal status, serum CA125 levels, and treatment approach) is able to predict patient response to first-line treatment with an AUC: 0.82 (95% CI 0.72 – 0.92).
Conclusion We have established a new strategy that combines molecular and clinical parameters to predict the response to first-line treatment in HGSC patients (HGSC-1LTR). This strategy can allow optimization of therapeutic decision making and individualize HGSC patients' care.

2022-RA-1574-ESGO APPLICATION OF *EX-VIVO* TUMOUR EXPLANT CULTURES TO PREDICT PLATINUM RESPONSES IN HIGH GRADE SEROUS OVARIAN CANCERS WITHIN A CLINICALLY RELEVANT TIMELINE

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Introduction/Background High grade serous ovarian cancer (HGSOC) management is based on maximal effort cytoreductive surgery and platinum chemotherapy. However, partly due to the high degree of heterogeneity in HGSOC, most patients will experience recurrent relapses and develop platinum resistance. In recent years, tumour models have been used to better understand HGSOC, particularly 3D patient-derived tumour models. *Ex-vivo* explant cultures preserve the tumour microenvironment and architecture, allowing more accurate study of tumour response to therapy. In this study, we develop a protocol for generating platinum sensitivity readouts of patient-derived *ex-vivo* explant culture within a clinically relevant period.
Methodology We generated *ex-vivo* explant cultures from tumours collected from chemo-naïve patients undergoing primary cytoreductive surgery for advanced disseminated HGSOC and treated with cisplatin for 48 hours. Immunohistochemistry was used to determine tumour content (PAX8, p53), and levels of proliferation (Ki67) and apoptosis (cleaved caspase-3). QuPath digital pathology software was used to quantify responses to cisplatin relative to untreated samples generated from the same tumour site.
Results Applying digital pathology to tumour explants allowed for reproducible and rapid quantification of proliferation and apoptosis markers to determine viability of explant cultures and apoptosis induction in response to drug treatments. We observed variations in responses to cisplatin treatments across patients (n=7) and multisite deposits within the same patient (n=3 patients, with 2–3 tumours each).
Conclusion *Ex-vivo* tumour explant cultures capture the heterogeneity of HGSOC and therefore are an ideal model for testing responses to platinum chemotherapeutics, targeted treatments or novel agents, and homologous recombination repair capacity. The use of multisite tumours confirms that intra-tumoural heterogeneity plays a role in responses to chemotherapy and emphasizes the value of multisite sampling for the study of HGSOC. From surgery to analysis, this method can be completed within 2–3 weeks, allowing it to be used to guide personalized chemotherapy regimens.

2022-RA-1582-ESGO INHIBITION OF THE WNT/β-CATENIN PATHWAY WITH DKK3 PROTEIN – A NEW VIRAL THERAPY FOR TREATMENT OF OVARIAN CANCER?

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Introduction/Background Wnt/β-Catenin signalling pathway plays an important role in many cellular processes, including cell proliferation. Abnormal functioning of the pathway has been demonstrated in ovarian cancer and therefore could be the focus for novel treatments, including viral therapies. In this study, we examined the effects of Wnt/β-Catenin pathway inhibition in ovarian cancer by infecting ovarian cancer cells with modified adenovirus 5 (Ad5) expressing Dickkopf-3 (DKK3) protein, a known Wnt/β-Catenin pathway inhibitor
Methodology DKK3 expression in the virus was confirmed by quantitative PCR test against DKK3 and other Wnt target genes and Western Blot. Once confirmed, 10k epithelial ovarian cancer cells (SKOV3 cell line) were infected with the modified virus at 1k, 2.5k, 5k and 10k virus particles per cell for CellTiter Glo (CTG) assay with results analysed at 24, 48 and 72hrs post infection. In Colony Forming Assay, 300 SKOV3 cells were infected at the same virus particles per cell ratios and analysed after 14 days. The same assays were performed with doxorubicin and Ad5RAD as positive and negative controls respectively.
Results CTG assay showed reduced cell viability and proliferation of cancer cells for the first 48hrs post infection. In the colony forming assay, ovarian cancer cells were able to form multiple colonies of more than 50 cells 2 weeks after viral suppression of the Wnt/β-Catenin pathway, indicating the inhibition may not have long standing effects on cancer cells' ability to grow and multiply.
Conclusion Our results indicate infecting cancer cells with Ad5 expressing DKK3 successfully inhibits the Wnt/β-Catenin pathway and leads to short-term reduction in cell proliferation. Further studies are needed to establish any long-term effects and potential translation into clinical practice.

2022-RA-1608-ESGO CLINICAL IMPLICATIONS OF GENOMIC INTRATUMOURAL HETEROGENEITY 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 a lack of predictive biomarkers means that matching the best treatment options to patients is difficult. This study aims to describe the extent of spatial and temporal ITH in advanced stage HGSOC at presentation and relapse and its implications for patient management.